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0723f6 homo sapien
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08bi4 homo sapien
01533 homo sapien
05336 homo sapien
0283f6 homo sapien
8c2wj6 homo sapien
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                                                                                                                                                                          1 GGVPGAIPGGVPGGVFYPGA.....LSPIFPGGACLGKACGRKRK 698
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8N2G0
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Q158W15
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Q17235
Q16014
AAH65566
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ALIGNMENTS

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Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P., Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D., "Isolated supravalvular aortic stenosis: functional haploinsufficiency of the elastin gene as a result of nonsense-mediated decay."; Hum. Genet. 106:577-588 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Skin fibroblast,
MEDLINE-89009960; PubMed=3171221;
MEDLINE-89009960; PubMed=3171221;
Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.,
"Cloning of full-length elastin cDNAs from a human skin fibroblast
recombinant cDNA library: further elucidation of alternative splicing
utilizing exon-specific oligonuclectides.";
J. Invest. Dermatol. 91:458-464(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green B.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M., "Cutis laxa arising from frameshift mutations in exon 30 of the
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE=87289668; PubMed=3039501;
MIDLINE=87289668; PubMed=3039501;
Rosenbloom J.C., Peltonna L., Rosenbloom J.,
"Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNN.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).";
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISOUR-FIRGCENTR;
MEDLINE-88156138; PubMed-2831431;
Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
Rosenbloom J., Uitto J.;
"Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keating M.T.;
"LIM-kinasel hemizygosity implicated in impaired visuospatial
constructive cognition.";
                                                  P15502; Q14233; Q14238; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) O1-APR-1990 (Rel. 14, Last annotation update) Elastin precursor (Tropoelastin).
                                          730 AA.
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                                          PRT;
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MEDLINE-96291399; PubMed-8689688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lab. Invest. 58:270-277(1988).
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                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 86:59-69(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblasts.";
                                        ELS HUMAN
                                                                                                                                                        Name=ELN;
                    ELS_HUMAN
RESULT 1
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Isold=P15502-2; Sequence=VSP 004243;

Isold=P15502-2; Sequence=VSP 004243;

Isold=P15502-2; Sequence=VSP 004243;

Isold=P15502-2; Sequence=VSP 004243;

Isold=P15502-2; Sequence of deaminated Lys.

Isold=P153700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased reslitence and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis.

CC manifestations, including pulmonary emphysema, bladder diverticula, pulmonary acceptant and pyloric stenosis.

CC ardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren Syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome contouring genes from chromosome band 7q11.23.

C1 involving genes from chromosome band 7q11.23.

Stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of confined aorta which can occur sporadically, as an autosomal condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005515; C:extracellular space; TAS.
GO; GO:0005201; E:extracellular matrix structural constituent; TAS.
GO; GO:0008281; P:ocell proliferation; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:0007585; P:respiratory gaseous exchange; TAS.
HINTERPLY; IPRO03379; LTOPOELASTIN.
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              Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                              IsoId=P15502-1; Sequence=Displayed;
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AAB17544.1; -
CAA33627.1; -
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HSSP; P50099; 1ZFJ.
Genew; HGNC:3327; ELN.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Cipperies: Outs orientalis aries, Ovis ammon aries (domestic sheep)
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Cipate: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
Cipacession: S59623, A4758
Rivauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; B.
Matrix Biol. 14, 635-641, 1994
A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
A;Reference number: S59623
A;Accession: S59623
A;Accession: S59623
A;Accession: S59623
A;Accession: B59623
A;Actatus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-770 cMAU>
A;Cross-references: UNIPROT:P11547
R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smi Arch. Blochem. Blophys. 241, 684-691, 1985
A;Reference number: A24758; MUID:85305763; PMID:3839997
A;Residues: 655-669,671-716,732-770 cYOO>
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;760-765/Disulfide bonds: #status predicted
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207 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF 266
                                                                              GAGAAGVI.PGVGGAGVPGVPGAI.PGI.GGI.AGVGTPAAAAAAAAAAAAKAAKYGAAAGLVPGG 300
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                                                                                                                                                            267 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAKAAKYGAAAGLVPGG
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A; Residues: 1-453,483-617,651-792 < FAZ>
A; Cross-references: EMBL: M6860; NID:99182061; PIDN:AAA52382.1; PID:9182062
A; Note: this sequence represents a composite of several splice forms
R; Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
A; Ditle: Isolation and characterization of human elastin cDNAs, and age-associated varia
A; Accession: A53891; MUID:88156138; PMID:2831431
A; Molecule type: mRNA
A; Molecule type:
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R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant A;Reference number: A30524; MUID:89009960; PMID:3171221
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Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cybecession: A32707; A33705; A33052, A33050, A3
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A,Residues: 1-500,507-792 <IND>
A,Residues: 1-500,507-792 <IND>
A,Cross-references: UNIPROT:09UMK5; GB:M16983; GB:J02948
A,Cross-references: UNIPROT:2: Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, J. Biol. Chem. 264, 8887-8891, 1989
A,Title: Characterization of the complete human elastin gene. Delineation of unusual fA,Reference number: A33705; MUD:89255358; PMID:2722804
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A;Map position: 7411.23-7411.23
C;Superfamily: elastin
C;Superfamily: elastin
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-792/Product: elastin #status predicted <MAT>F;1-26/Domain: signal sequence #status predicted <MAT>F;782-787/Disulfide bonds: #status predicted
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Pred. No. 6.2e-154;
0; Mismatches 0;
                                                                                                                                                                                           elastin precursor, long splice form - human
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698; Conservative
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Matches 698; Conserv
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A;Molecule type: DNA
A;Residues: 1-27 <BAS>
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A;Gene: GDB:ELN
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November 19, 2004, 16:37:11; Search time 113.997 Seconds (without alignments) 2168.321 Million cell updates/sec
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| cgn2 \( \frac{6}{\} \) prodata/2/pubpaa/USO7 PUBCOMB.pep:*
| cgn2 \( \frac{6}{\} \) prodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2 \( \frac{6}{\} \) prodata/2/pubpaa/USO6 \( \true{NEW_PUB.pep:*} \)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1570615 seqs, 354127592 residues
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Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 1 2 3 3 3 3 3 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1	Score 3502 3578.5 3486.5 3486.5 3233.5 2931.5 1155 1156.5	% Match Matc	Ouery March Length DB ID 99.6 731 10 UG 99.0 731 15 UG 99.1 731 15 UG 99.4 663 15 UG 89.4 663 15 UG 81.6 617 14 UG 31.9 965 16 UG 31.9 965 16 UG 31.5 096 16 UG	DB 100 115 115 115 115 116	US-09-961-403-8 US-09-961-403-8 US-09-964-662-1 US-10-210-172-38 US-10-108-266A-2477 US-10-108-266A-2477 US-08-806-029-28 US-08-806-029-28 US-08-806-029-26 US-08-806-029-26	Description Sequence 8, Appli Sequence 1, Appli Sequence 18, Appli Sequence 2477, Appl Sequence 2477, Appl Sequence 2915, Appl Sequence 28, Appl Sequence 27, Appl Sequence 27, Appl
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sequence 15, sequence 19, sequence 19, sequence 15, sequence 35, sequence 36, sequence 36, sequence 14, sequence 31, sequence 31, sequence 34, sequence 35, sequence 35, sequence 36, sequence 36, sequence 34, sequence 35, sequence 36, seque	100
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us-09-743-818a-5.rapb

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Sequence 1, Application US/09964662
| Publication No. US20031066846A1
| GENERAL INFORMATION:
| APPLICANT: PROTEIN SPECIALITIES LTD.
| APPLICANT: PROTEIN SPECIALITIES LTD.
| APPLICANT: PROTEIN SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND ITILE OF INVENTION: SILF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND FILE REFERENCE: 041082/0112
| CURRENT APPLICATION NUMBER: US/09/964,662
| CURRENT FILING DATE: 2003-05-08
| PRIOR APPLICATION NUMBER: 09/340,736
| PRIOR PRILING DATE: 1999-06-29
| NOMBER OF SEQ ID NOS: 11
| SOFTWARE: PATENTIN VEF. 2.1
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        387 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGGSPEAQAAAA 446
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                                     421 AKAAKYGVGTPAAAAKAAAKAAQF-----GLVPGVGVAPGVGVAPGVGVAPGVGLAPG
                                                                                                    V.G.V.A.P.G.V.G.V.A.P.G.I.G.P.G.C.V.A.A.A.K.S.A.K.V.A.K.A.Q.L.R.A.A.G.I.P.G.L.G.V.G.V.G.V.P.
                                                                                                                  507 VGVAPGVGVAPGGGVAAPGIGPGGVAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVP
                                                                  447 AKAAKYGVGTPAAAAAAAAAAAGFALLINLAGLIVPGVGVAPGVGVAPGVGVAPGVGLAPG
                                                                                                                                                            GLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVG
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Matches 696; Conservative
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ORGANISM: Homo sapiens
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                    Sequence 24,
Sequence 34,
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99.1%; Pred. No. 5.6e-186;
ive 0; Mismatches 0; Indels 6
                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09961403

Publication No. US20030077589A1

GENERAL INFORMATION:

APPLICANT: H-STUMPP, HOLGER

APPLICANT: HAENDLER, BERNARD

APPLICANT: KRETZSCHMAR, JOERN

APPLICANT: KRETTSCHMAR, JOERN

APPLICANT: REGIDOR, PEDRO

APPLICANT: REGIDOR, PEDRO

TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDO

FILE REFERENCE: SCH-1789

CURRENT APPLICATION NUMBER: US/09/961,403

CURRENT FILING DATE: 2001-09-25

NUMBER OF SEG ID NOS: 15
4 US-10-414-760-14

US-08-806-024

US-08-806-029-34

4 US-10-414-760-13

4 US-10-414-760-13

4 US-10-414-760-22

6 US-10-720-025-61

US-09-861-597-1

4 US-10-414-760-1

4 US-10-414-760-1

5 US-10-441-965-25

5 US-10-424-599-269890

6 US-10-096-986-98

6 US-10-096-986-98

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6 US-10-369-493-7032
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Aay 69068 Amino aci
Aab 66657 Human ela
Abg 72223 Human ela
Abg 72223 Human ela
Abg 18222 Human ela
Aav 18222 Human ela
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AAR8025 ABP5347 AAY3168 AAR8025 ABP5347 AAR832 AAR101 AAW352 AAW352 AAW5352 AAW5352 AAW5352	ABG69272 AD69213 AAW52541 AAW603213 AAW52541 AAW49728 AAX51882 AAX51882 AAX51882 AAX51882 AAX60335 AAR60335 AAR60335 AAR60335 AAR60335 AAR60238 AAR60238 AAR60238 AAR60218 AAV551888 AAV551888 AAX782544 AAX51888 ABG31418 AAX51888 ABG31418 AAX51855 AAR80256 AAR80256 ABF53477 AAR80256 ABF53461 AAR80256 ABF53461 AAR80256 ABF53461 AAR80256	AAY7828 AD846927 AD846927 ABF3347 AAW78188 ABG3142 AAW78189 ABG3142 ABG3142 ABG3142 ABG417 ABG417 ABG6927 AAY7828 AAY7828 AAY7828 AAY7828
9988 745 832 932 932 932 932 932 932 932 932 932 9	22.22.22.22.22.22.22.22.22.22.22.22.22.	00055 00055 00055 00055 00055 00055 00055 00055 00055 00055 00055 00055 00055 00055 00055
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121 FAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGYGPGGVA-AAGKAGYP 179
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pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                 180 TGTGVGPQAAAAAAAAKAAAKFGAGAAGFGAVPGVGGAGVPGVPGAIPGIGGIAGVGTPAA
                                                                                                                                                   240 AAAAAAAAKAAKYGAAAGLVPGGPGFGBCVVGVPGFGAVPGVGVPGAGIPVVPGAGIPGA
                                                                                                                                                                                                                                                                                                                                                                          VGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRA
                                                                                                                                                                                                           301 AGFGAVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFFGFGVGVGGIPGVAGVPS
                                                                                                                                                                                                                                                                                          VGGVPGVGGVPGVGISPEAQAAAAAAAKAAKYGVGTPAAAAAAAAAAAAAQFGLVPGVGVAPG
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                                                                                                                            241 AAAAAAAKAAKYGAAAGLVPGGPGFGPGVVGVPGFGAVPGVGVPGAGIPVVPGAGIPGA
                                                                                                                                                                                                                                                  300 AGFGAVSPEAAAKAAKAAKYGARPGVGVGGIPTYGVGAGFFPGFGVGVGGIPGVAGVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAVPGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGIPGVGPPGGPQPGVPLGYPIXAPKLPGGVGLPYTTGKLPYGYGPGGVACAAGKAGYP 180
  Aaw53521 Amino aci
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                                                                                                                                                                                                                                                                                                                                              Tropoelastin, hTE; elastin, glycosaminoglycan; GAG-binding, medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGGVPGAVPGGVPGGVFYPGAGFGAVPGGVADAAAYKAAKAGAGLGGVPGVGGLGVSAG
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                                                                                                                                                                                                                                                                                                         Human tropoelastin derivative SHELdeltamodified.
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                                                                                   ALIGNMENTS
  AAW53521
AAY31680
                                                                                                                                                                                   AAY01303 standard; protein; 660 AA
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2107
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27.2
27.1
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November 19, 2004, 16:37:11 ; Search time 107.954 Seconds (without alignments) 2168.321 Million cell updates/sec
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1 MGGVPGAVPGGVPGGVFYPG.....LSPIFPGGACLGKACGRKRK 661
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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 8, Appli	Sequence 1, Appli	Sequence 38, Appl	Sequence 40, Appl	Sequence 2477, Ap	Sequence 2915, Ap	Sequence 28, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 27, Appl	Sequence 29, Appl	Sequence 31, Appl	Sequence 82, Appl
	ID	US-09-961-403-8	US-09-964-662-1	US-10-210-172-38	US-10-210-172-40	US-10-108-260A-2477	US-10-104-047-2915	US-08-806-029-28	US-09-837-969A-38	US-09-841-321A-38	US-08-806-029-27	US-08-806-029-29	US-10-800-179-31	14 US-10-096-986-82
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us-09-743-818a-6.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 19, 2004, 16:06:25; Search time 29.7306 Seconds (without alignments) 2139.188 Million cell updates/sec

US-09-743-818A-6 3426 1 MGGVPGAVPGGVFGVFYPG......LSPIFPGGACLGKACGRKRK 661 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 s

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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QY         26        VPGGVADAAAAYKAAKAGAGLGCVPGVGGLGVSAGAVVPQPCAGGVKPGKVPGVGL         80           BY         FPGALVPGGVADAAAAXKAAKAGGLGGVPGVGGLGVSAGAVVPQPCAGCKVPGVGL         146           CY         81         PGVYPGGARPFGVGVLPGVPTGAGVKPKAPGVGGAPAGTPGVGPFGGPQPVPLG         140           CY         81         PGVYPGGARPFGAGVGVLPGVPTGAGVKPKAPGVGGAPAGTPGTGVGPFGGPQPQPLG         140           Db         147         PGVYPG-GVLPGARFFGVGVLPGVTGAGVKPKAPGVGGAPAGTPGTGVGPPGGPQPQPCPLG         205           QY         141         YPIKAPKLPGGYGLPYTTGKLPYGGVRGAGARGAGAPGTGTGVGPQAAAAAAAAAAA         200	C;Keywords: al C;760-765/Disu Query Match Best Local S Matches 524 Oy 2	s: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine //Disulfide bonds: #status predicted ADISULFIDE DONE
	}	GOVEGOV FGGV FF FGAGEGGEGGEGGEGGVARARGGGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEG



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
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MEDLINE=99091639; PubMed=9873040;
Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
"Cutis laxa arising from frameshift mutations in exon 30 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosembloom J., Uitco J., "Isolation and characterization of human elastin cDNAs, and ageassociated variation in elastin gene expression in cultured skii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "LIM-kinase1 hemizygosity implicated in impaired visuospatial constructive cognition.";
                                                                                    P15502; 014233; 014238;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                             730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hippocampus, and Placenta;
MEDLINE=96291399; PubMed=8689688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88156138; PubMed=2831431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 274:981-986(1999).
                                                                                                                                                                                                                  Elastin precursor (Tropoelastin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lab. Invest. 58:270-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 603-730 FROM N.A.
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVEMENT IN SVAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 86:59-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastin gene (ELN)
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10942104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keating M.T.
                                                          ELS HUMAN
                                                                                                                                                                                                                                                  Name=ELN;
RESULT 1
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Isold=F15502-2; Sequence=VSP 004243;

Isold=F15502-2; Sequence=VSP 004243;

Isold=F15502-2; Sequence=VSP 004243;

Isold=F1878: Defects in ELN are a cause of autosomal dominant cutis laxa [MIW:123700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis.

-!- DISEASE: Haploinsufficiency of ELN may be the cause of certain validowascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194056]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23. Valvalvular aortic stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal deminant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005515; C:extracellular space; TAS.
GO; GO:00055015; C:extracellular matrix structural constituent; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:0009867; P:organogenesis; TAS.
GO; GO:0007885; P:respiratory gaseous exchange; TAS.
InterPro: IPRO03979; tropoelastin.
PRINTS; PRO1500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
Structural protein; Williams-Beuren syndrome.
              Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                              [soId=P15502-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC98394.1; JOINED.
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AAC98394.1; JOINED.
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AAA53190.1; -...
AAB17544.1; -...
CAA33627.1; -...
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EMBL; M16983; AAC98394.1;
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AAC98394.1;
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 ALTERNATIVE PRODUCTS:
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Genew; HGNC:3327; ELN.
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M17273;
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                                                                                                                   November 19, 2004, 16:06:25; Search time 0.584716 Seconds (without alignments) 2139.188 Million cell updates/sec
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5.1.6
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
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A; Reference number: S59623

## ALIGNMENTS

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R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smit
Arch. Blochem. Blophys. 241, 684-691, 1985
A;Hitle: Analysis of the 3' region of the seep elastin gene.
A;Reference number: A24758; MUID:85305763; PMID:3839997
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A;Residues: 1-864 <PIE>
A;Cross-references: UNIPROT:Q99372; GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1;
                                                                                                                                                                                                                                                                                              A;Accession: A24758
A;Molecule type: mRNA
A;Residues: 655-669,671-716,732-770 <YOO>
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;760-765/Disulfide bonds: #status predicted
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C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-27-Domain: signal sequence #status predicted <SIG>
F;28-860/Product: elastin #status predicted <MAT>
F;850-855/Disulfide bonds: #status predicted
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R,Wdiner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A;Title: Use of an intron length polymorphism to localize the tropoelastin gene to A;Reference number: A55721; MUID:95130069; PMID:7829060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
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Cibate: 11-Jan-1991 #sequence revision 16-Aug-1996 #text change 09-Jul-20
Cibate: 11-Jan-1991 #sequence revision 16-Aug-1996 #text change 09-Jul-20
CiAccession: A36106; A30818; A36523; S02103; 154172; 168505
R;Pierce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
Biochemistry 29, 9677-9683; 1990
A;Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.
A;Reference number: A36106; MUID:91104868; PMID:1702999
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Pred. No. 0.19;
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Pred. No.
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                                                                                           A;Residues: 1-770 <MAU>
A;Cross-references: UNIPROT:P11547
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92.3%;
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92.3%;
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N;Alternate names: tropoelastin
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N;Alternate names: tropoelastin
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                            A; Status: preliminary; not
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Best Local Similarity
Matches 12; Conserv
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A;Residues: 1-860 <WYD>
                                                            A; Molecule type: mRNA
S59623
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A; Accession:
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A,Residues: 164-453,483-500,507-617,651-792 <FA2>
A,Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-500,507-792 <IND>
A;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
A;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W. J. Biol. Chem. 264, 8887-8891, 1989
A;Title: Chem. 264, 8887-8891, 1989
A;Title: Characterization of the complete human elastin gene. Delineation of unusual fea A;Reference number: A33705; MUID:89255358; PMID:2722804
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R;Fazio, M.J.: Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N. J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of Full-length elastin cDNAs from a human skin fibroblast recombinant of A;Reference number: A30524; MUID:89009960; PMID:3171221
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A;Reference number: A53891; MUID:88156138; PMID:2831431
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                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 22-Unn-1990 Hasquence revision 26-Unl-1996 #text_change 09-Unl-2004
C;Date: 22-Unn-1990 Hasquence revision 26-Unl-1996 #text_change 09-Unl-2004
C;Accession: A32707; A33705; A30524; A53891
R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, Proc. Natl. Acad. SGI. U.S.A. 84, S680-5684, 1987
A;Title: Alternative splicing of human elastin mnAx indicated by sequence analysis of A;Reference number: A32707; MUID:87289668; PMID:3039501
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C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59623, A24758
R;Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.;
Matrix Biol. 14, 635-641, 1994
A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
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A;Map position: 7q11.23-7q11.23
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-792/Product: elastin #status predicted <MAT>
F;782-787/Disulfide bonds: #status predicted
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R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom,
Lab. Invest. 58, 270-277, 1988
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A;Residues: 1-453,483-617,651-792 <FAZ>
A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 59; DB 1;
; Pred. No. 0.028;
0; Mismatches 0
                                                                                                                               elastin precursor, long splice form - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                                                               N;Alternate names: tropoelastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 ALAAKAAKYGAA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALAAAKAAKYGAA 13
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A; Residues: 1-27 <BAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ine oxidase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A33705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A30524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A53891
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Alternate names: tropoelastin
C;ppecies: dallus gallus (chicken)
C;ppecies: dallus gallus (chicken)
C;ppecies: 05-Oct-1988 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A26601; A30795; A27264
R;Bressan, G.M.; Axgos, P.; Stanley, K.K.
Biochemistry 26, 1497-1503, 1987 thick tropoelastin revealed by complementary DNA cloning.
A;Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 678-683, 685-747 <ROS>
A; Tross=references: GB:M31, 685-747 <ROS>
A; Tross=references: GB:M31, 685-747 <ROS>
A; Tross=references: GB:M31, 686-747 <ROS
A; Tross=references: GB:M31, 686-747 <ROS
B; Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
B; Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
B; Brown, B:Dophys. Res. Commun. 186, 549-555, 1992
A; Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an int A; Reference number: A5661; MUID:92337651; PMID:1632791
A; Rontents: annotation, disulfide bonds
C; Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
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Fi27-747/Product: elastin #status predicted <MAT>
Fi105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,68E
Fi737-742/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1,7ES',4-11,7E',13-225,260-636,7V',638-747 <RA3>
A;Residues: 1,7ES',4-11,7E',13-225,260-636,7V',638-747 <RA3>
A;Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
R;Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenblc Biochemistry 24, 3075-3080, 1985
A;Tible: Structure of the 3' portion of the bovine elastin gene.
A;Reference number: A22343; MUID:85280426; PMID:2992576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A;Reference number: 145885; MUID:85059254; PMID:6150137
A;Accession: 145886
                                                       c deduced from the sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
A;Note: the list of introns is incomplete
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1.747/Product: elastin precursor, splice form a #status predicted <BPA>
F;1.225,260-747/Product: elastin precursor, splice form c #status predicted <BPB>
F;1.225,240-747/Product: elastin precursor, splice form b #status predicted <BPB>
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                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-636,'V',638-747 <RAJ>
A;Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
A;Accession: B26728
                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1, RS', 4-11, B', 13-225, 240-636, VV', 638-747 <RA2>
A;Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026
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                   J. Biol. Chem. 262, 5755-5762, 1987
A;Title: Primary structures of bovine elastin a, b, and A;Reference number: A92640; MUID:87194772; PMID:3032943
A;Accession: A26728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 613-747 <CIC>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
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NyAlternate names: tropoelastin
NyAlternate names: tropoelastin
NyContains: elastin precursor, splice form b; elastin precursor, splice form c
C;Species: Bos primigenius taurus (cattle)
C;Date: Os-Jun-1999 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A31865; A26728; B26728; A26728; A26728; I45886
R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams, Biochemistry 28, 2365-2370, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          άs
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R;Franzblau, C.; Pratt, C.A.; Faris, B.; Colannino, N.M.; Offner, G.D.; Mogayzel Jr., P. Biol. Chem. 264, 15115-15119, 1989
A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells. A;Reference number: A36523; MUID:89359327; PMID:2768256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1; A; Note: the list of introns may be incomplete C; Superfamily: elastin (c; Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine F; 1-21/Domain: signal sequence #status predicted <SIG> F; 22-864/Product: elastin #status predicted <MAT> F; 854-859/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Experimental source: heart
R.Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
Genomics 12, 651-689, 1992
A.Ticle: Elements of the rat tropoelastin gene associated with alternative splicing.
A.Reference number: 154172; MUID:92241859; PMID:1572637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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A;Residues: 558-864 <RE2>
A;Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
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R,Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D. J. Biol. Chem. 263, 13504-13507, 1988
J-Jitle: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA. A; Reference number: A30878; MUID:88330868; PMID:2971041
A; Accession: A30878
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Arch. Biochem. Biophys. 268, 551-558, 1989
A;Title: Characterization of rat heart tropoelastin.
A;Reference number: S02173; MUID:89117149; PMID:2913947
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Pred. No. 0.32;
0; Mismatches
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A,Residues: 'IP',369-545,548-764,770-864 <RIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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92.3%;
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                                                                                                                                                                                                                                                                               A; Residues: 781-864 < DEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 22-31 < FRA>
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Best Local Similarity
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A; Residues: 1-27 <YEH>
                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A31865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: I68505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: I54172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A36523
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A,Residues: 1-375 <KUR>
A,Residues: 1-375 <KUR>
A,Cross-references: UNIPROT:Q8U7E1; GB:AE008689; PIDN:AAL45302.1; PID:g17742991; GSPDB:CA,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AGR L 720 [imported] - Agrobacterium tumefaciens (strain C58, Cereo C; Species: Agrobacterium tumefaciens C; Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004 C; Accession: D98176 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004 C; Accession: D98176 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004 P; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., A: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., A: Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-375 <KUR>
A;Cross-references: UNIPROT:Q8U7E1; GB:AE007870; PIDN:AAK88934.1; PID:g15158710; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable lytic murein transglycosylase (N-term. LysM motif repeat domain) CAC1232 [impor Cispecies: Clostridium acetcbutylicum (cispecies: Clostridium acetcbutylicum (cispecies: Clostridium acetcbutylicum (cispecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (cispecies) as 187062 (cispecies) as 187062 (cispecies) as 1870011189, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. (cispecies) as 2001 (cispecies) as 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-253 -KUR>
A;Cross-references: UNIPROT:Q97JF1; GB:AE001437; PIDN:AAK79204.1; PID:g15024157; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
                            ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Pred. No.
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75.0%;
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75.0%;
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Best Local Similarity
-heq 9; Conserve
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                       A,Status: preliminary A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                           A; Accession: AH3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: Atu4508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A;Gene: AGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 85-784 <BAU>
A; Residues: 85-784 <BAU>
A; Residues: 85-784 <BAU>
A; Cross-references: GB: M21880; NID: 9212741; PIDN: AAA49082.1; PID: 9212742
B; Tokimitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.
Arch. Biochem. Biophys. 256, 455-461, 1987
A; Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcri
A; Reference number: A27264; MUID: 87297534; PMID: 3502711
                A;Molecule type: mRNA
A;Residues: 1-212,237-524,535-784 <BR2>
A;Cross-references: UNIPROF:P07916; GB:M15889; NID:g212803; PIDN:AAA49108.1; PID:g212804
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2361

A;Status: preliminary

A;Status: preliminary

A;Residues: 1-382 <KUR>
A;Residues: 1-382 <KUR>
A;Cross-references: UNIPROT:08YNW3; GB:BA000019; PIDN:BAB76147.1; PID:g17133584; GSPDB:GC;Genetics: A;Agene: alr448
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C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C,Accession: AH3110
R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A27264
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: MSNA
A;Rolecule type: MSNA
A;Rolecule type: MSNA
A;Rolecules type: MSNA
C;Superfamily: elastin
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C;Superfamily: Bacillus endo-beta-1,4-xylanase; Streptomyces endo-1,4-beta-xylanase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extracellular matrix; glycoprotein; hydroxylysine
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprote
F;1-24/Domain: signal sequence (fragment) #status predicted <SIG>
F;25-212,237-524,535-784/Product: elastin #status predicted <MAT>
F;773-779/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                             R;Baule, V.J.; Foster, J.A.
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988
A;Title: Multiple chick tropoelastin mRNAs.
A;Reference number: A30795; MUID:88309083; PMID:2841924
A;Accession: A30795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 2;
Pred. No. 0.94;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endo-1,4-beta-xylanase [imported] - Nostoc sp.
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1 Similarity 91.7%;
11; Conservative
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 9; Conserv
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2;

Score 39; DB 2 Pred. No. 25; 3; Mismatches

66.1%; 66.7%;

8; Conservative 1 ALAAAKAAKYGA 12

Query Match Best Local Similarity Matches 8; Conserv

A, Gene: CAC1232

:|:|||||| ||: 207 SLSAAKAALYGS 218

RESULT 11 D42653

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hypothetical protein PH1302 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: F71000
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
R;Kawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA, Res. S, S5-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Accession: F71000
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-860 «KAW
A;Residues: 1-860 «KAW
A;Residues: 1-860 «KAW
A;Coss-references: UNIPROT:O59003; GB:AP000006; NID:g3236133; PIDN:BAA30406.1; PID:d1031
A;Ross-references: UNIPROT:O59003; GB:AP000006; NID:g3236133; PIDN:BAA30406.1; PID:d1031
A;Ross-references: Uniprocession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin binding, heterododecamer; ligase; mitochondrial matrix; mitochondrion F;1-27/Domain: transit peptide (mitochondrion) (fragment) #status predicted <TNP> F;28-704/Product: propionyl-CoA carboxylase alpha chain #status predicted <MAT> F;41-492/Domain: biotin carboxylase homology <ECH> F;631-704/Domain: lipoyl/biotin.binding homology <LPB> F;631-704/Domain: lipoyl/biotin.binding homology <LPB> F;670/Binding site: biotin (Lys) (covalent) #status predicted
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 11-Jan-2002 C; Accession: A34337, A30871  
F; Srowner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E. J. Biol. Chem. 264, 12680-12685, 1989  
A; Title: Sequence analysis, biogenesis, and mitochondrial import of the alpha-subunit of A; Reference number: A34337; MUID:89308706; PMID:2745462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: annotation; correction
A;Note: the first 17 residues in the original paper were derived from bacterial DNA as
C;Genetics:
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A,Accession: A30871
A,Molecule type: mRNA
A,FRESidues: "MPYRERFCAIRWCRNSG',1-298,'WP',301-704 <BR2>
A,Cross-references: GB:M22631; NID:g206049; PIDN:AAA88512.1; PID:g206050
A,Cross-references: GB:M22631; NID:g206049; PIDN:AAA88512.1; PID:g206050
B,Enowner: M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.
J. Biol. Chem. 266, 4660, 1991
A,Reference number: A43040
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Pred. No. 93;
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66.7%; Pred. No. 1.1e+02;
ive 0; Mismatches 4,
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                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 'MPYRERFCAIRWCRNSG',1-704 <BR1>
A,Cross-references: GB:M22631
R;Browner, M.F.; Taroni, F.; Sztul, E.; Ross
submitted to GenBank, February 1989
A;Reference number: A30871
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Best Local Similarity
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Best Local Similarity
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Cispecies: Acessaion: D42653

R;Wallbrandt, P.; Tegman, V.; Jonsson, B.H.; Wieslander, A.

J. Bacteriol. 174, 1388-1396, 1992

A;Reference number: A42653; MUID:92138635; PMID:1735725

A;Accession: D42653

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Succinylglutamic semialdehyde dehydrogenase [imported] - Caulobacter crescentus
C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: F87448
R; Niserman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Dukkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
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C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
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Pred. No. 33;
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2; Mismatches

66.1%; 72.7%;

Query Match
Best Local Similarity 72.,
-Lag 8; Conservative

2 LAAAKAAKYGA 12 VAAIKAAQYGA 28

à q RESULT 12

15

RESULT 833422

propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - rat (fragment) C.Species: Rattus norvegicus (Norway rat)

A34337

66.1%; Score 39; DB 2; 72.7%; Pred. No. 45; ive 1; Mismatches

|||||| | :|| ||ALAAANATRYG 401

1 ALAAAKAAKYG 11

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Best Local Similarity Matches 8; Conserv

Query Match

A; Residues: 1-485 <STO>

C, Genetics

A; Status: preliminary A; Molecule type: DNA

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A;Residues: 1-252 <NRN>
A;Residues: 1-252 <NRN>
A;Cross-references: UNIPROT:Q08383; GB:L06254; NID:g310272; PIDN:AAA71911.1; PID:g310276
A;Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBIP:131920)
C;Superfamily: Molybdate-binding periplasmic protein ModA
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A;Experimental source: strain R1
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K;Konsolaki, M.; Komitopoulou, K.; Tolias, P.P.; King, D.L.; Swimmer, C.; Kafatos, F.C.
Nucleic Acids Res. 18, 1731-1737, 1990

A;Title: The chorion genes of the medfly, Ceratitis capitata, I: structural and regulato
A;Reference number: S09208; MUID:90245561; PMID:1692403
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: G75468
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Namathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S: Smith, H.O.; Venter, J.C.; Fraser, C.M.
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C;Date: 29-Jan_1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
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Pred. No. 55;
2; Mismatches 3; Indels
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              A; Reference number: A36914; MUID:93259949; PMID:8491722
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Pred. No. 68;
1; Mismatches
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Pred. No. 6
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61.5%;
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135 AIADPKSAPYGAA 147
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Matches 8; Conservative
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Matches 8; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <WHI>
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Best Local Similarity
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A; Residues: 1-320 <KON>
                                                                         A;Status: preliminary A;Molecule type: DNA
                                             A;Accession: E36914
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                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cipecies: Sinorhizobium meliloti
Ribarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
Ribarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
Nacl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A.Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A.Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A.Factus: preliminary
A.Reference number: A95262; MUID:21396509; PMID:11484432
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-244 «KUR»
A.Factus: preliminary
A.Residues: UNIPROT: Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
A.Status: preliminary
A.Residues: UNIPROT: Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
A.Status: preliminary
A.References: UNIPROT: Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
A.Factus: preliminary
A.Residues: UNIPROT: Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
A.Factus: Preliminary
A.References: UNIPROT: Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
A.Factus: A.Fact
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P36892; EMBL:Z19594; NID:g298046; PIDN:CAA79646.1; PID:g5753
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C;Species: Rhodobacter capsulatus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: E36914
R;Wang, G; Angermuller, S.; Klipp, W.
J. Bacteriol. 175, 3031-3042, 1993
A;Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SMa0013 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
                                                                                                                                               Σ
                     Cypecies: Streptonyces ambofactens
Cybecies: Streptonyces ambofactens
Cybecession: S33422
CyAccession: S33422
Submitted to the EMBL Data Library, January 1993
AyDescription: Identification of a gene encoding the replication initiator protein of the AyAccession: S33422
AyAccession: S33422
AyAccession: S33422
AyAccession: Library
AyAccession: S3422
AyAccession: S3422
AyAccession: S3442
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hypothetical protein 183 - Streptomyces ambofaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2;
Pred. No. 41;
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61.5%; Pred. No.
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ilarity 75.0%;
Conservative
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Matches 8; Conservative
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Best Local Similarity
Then 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon: GTG
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ccetyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus halodurans cretyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus halodurans c.Species: Bacillus halodurans c.Species: D1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 c.Accession: C83998 h.7 Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c.A.Reference number: A83650; MUID:20512582; PMID:11058132 h.A.Ccession: C83998 h.A.A.Residues: preliminary A.Molecule type: DRA A.Residues: 1-452 c.STO A.Residues: 1-452 c.STO A.Residues: L452 c.STO A.Residues: L452 c.STO A.Residues: L452 c.STO A.Residues: Strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 393, 537-544, 1998

Alathors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome the A; Accession: G70693

A; Accession: G70693

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-439 < COL>
A; Cross-references: UNIPROT: P71616; GB: Z81331; GB: AL123456; NID: G3261650; PIDN: CAB03650.1

A; Experimental source: strain H37RV
                                                                                              A;Cross-references: UNIPROT: O8X726; GB:AE005174; NID:g12518888; PIDN:AAG59165.1; GSPDB:GA;Experimental source: strain 0157:H7, substrain EDL933 (Genetics: A;Genetics: A;Gene: Z5522 C;Superfamily: hippurate hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable dinF protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: G70693

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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Pred. No. 93;
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                                                                                                                                                                                                                                                                             Length 388;
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A,Gene: accC
C,Superfamily: biotin carboxylase; biotin carboxylase homology
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2; Mismatches
                                                                                                                                                                                                                                                                                Score 37;
Pred. No.
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61.5%;
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nilarity 66.7%;
Conservative 2
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Best Local Similarity 72.,
8; Conservative
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252 AAAVAARFGAA 262
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Best Local Similarity
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Les 8; Conserv
                                                                                     A;Residues: 1-388 <STO>
A;Accession: A86088
A;Status: preliminary
A;Molecule type: DNA
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Matches
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A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                               C.parellers: fylocolus molinosini
C.parellers: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C.Accession: E71201
R.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
R.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A.; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT:05937; GB:AP000007; NID:g3236134; PIDN:BA31004.1; PID:g323 A; Experimental source: strain OT3 A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable amino acid amidohydrolase [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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A,Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: D91240
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D91240
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                                                                                                                probable glucose-fructose oxidoreductase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2
Pred. No. 71;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.7%; Score 37; DB 66.7%; Pred. No. 81; cive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: ECs4892
C;Superfamily: hippurate hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%;
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ALAQAQAASFGA 284
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-388 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: PH1882
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photosystem II chlorophyll a-binding protein psbB precursor - Prochlorothrix hollandica NiAlternate names: photosystem II CP-47 protein C;Species: Prochlorothrix hollandica C;Species: Prochlorothrix hollandica C;Date: 30-Uun-1992 #sequence_revision 30-Uun-1992 #text_change 09-Jul-2004 C;Accession: S17739 #ssquence_revision 30-Uun-1992 #text_change 09-Jul-2004 C;Accession: S17739 #s.S. S. Plant Mol. Biol. 17, 915-917, 1991 A;Tile: Nucleotide sequence of psbB from Prochlorothrix hollandica.
                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-514 <GRE>
A,Cross-references: UNIPROT:P27200; EMBL:X59614; NID:g45537; PIDN:CAA42177.1; PID:g45538
A,Note: the authors translated the codon CCC for residue 134 as O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N2,N2-dimethylguanosine tRNA methyltransferase - fission yeast (Schizosaccharomyces pomb C;Species: Schizosaccharomyces pombe C;Species: 30-Bec-1999 #sequence_revision 03-Bec-1999 #text_change 03-Bec-1999 C;Accession: T39993 #sequence_revision 03-Bec-1999 #typne, M.; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Churcher, submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA (quanine-N2-)-methyltransferase (EC 2.1.1.32) [imported] - fission yeast (Schizosac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524 «LYN»
A;Cross-references: EMBL:AL031158; PIDN:CAA20101.1; GSPDB:GN00067; SPDB:SPBC25D12.05
A;Experimental source: strain 972h-; cosmid c25D12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: chlorophyll; photosynthesis; photosystem II; transmembrane protein F;19-40/Domain: transmembrane #status predicted <TM1>
F:104-120/Domain: transmembrane #status predicted <TM2>
F:146-162/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 09-Jul-2004
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Pred. No. 1e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: psbB
C;Superfamily: photosystem II chlorophyll a-binding protein
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F;245-261/Domain: transmembrane #status predicted <TM5>
F;459-475/Domain: transmembrane #status predicted <TM6>
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C'Date: 18-Feb-2000 #sequence_revision 18-Feb-2000
C'Accession: T46565
R'Niederberger, C.
submitted to the EMBL Data Library, February 1998
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: SPDB:SPBC25D12.05
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Best Local Similarity
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Matches 8; Conserv
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R;Barnett, M.J; Fisher, R.F; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows F; Kalman, S; Kaating, D.H; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Recession: E95367
A;Residues: Preliminary
A;Mocession: E95367
A;Residues: 1-453 «KUR>
A;Residues: 1-453 «KUR>
A;Residues: 1-453 «KUR>
A;Residues: UNIPROT:Q92XW8; GB:AE006469; PIDN:AAK65503.1; PID:g14523976; GSPDB:GA:Residues: UNIPROT:Asimon, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Pinan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Hyman, R.W.; Jones, T.
Science 293, 688-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.U.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A.; A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable aldehyde dehydrogenase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Bate: 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36807
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Oliver, C. Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B;Diver, C. Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Oliver, E. Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Recence number: Z21614
A;Recence number: Z21614
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: L-462 cOil.>
A;Resperimental source: strain A3(2)
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                            - Sinorhizobium meliloti (strain 1021
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                                                                                                                                                                                                                                                                probable methyltransferase - chemotaxis [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
      Gaps
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      Indels
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      4,
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Pred. No. 93;
0; Mismatches
   Mismatches
   1;
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                                                                                                                     259 AVAAKAVNYSGA 271
                                                        1 ALAAAKAAKYGAA 13
Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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297 SLAAEAAKYG 307
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Best Local Similarity
Matches 8; Conserv
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A;Genome: plasmid
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Matches
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Probable membrane protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Nycobacterium leprae
C;Species: Nycobacterium leprae
C;Saccession: A86301
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Cole, S.T.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, A;Hitle: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MulD:21128732; PMID:11234002
A; Description: Cloning and characterization of the putative tRNA (guanine-N2-)-methyltra A; Reference number: Z23073
A; Recession: T46565
A; Accession: T46565
A; Roctus: prelimary, translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-548 <NIE>
A; Cosser-references: UNIPROT:Q9P804; EMBL:AJ224000; PIDN:CAA11801.1
C; Genetics:
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A;Molecule preliminary
A;Molecule 1-902 <STO>
A;Cross-references: GB:AL450380; NID:g13092515; PIDN:CAC29645.1; GSPDB:GN00147
C;Genetics:
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ALIGNMENTS

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472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
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Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
Duronio V., Koop B.F.;
"Comparative genomic sequence analysis of the Williams syndrome region
(LIMK1-RFC2) of human chromosome 7q11.23.";
Mamm. Genome 11:890-898(2000).
EMB1: U63721; AAC13884.1;
InterPro; IPR001451; Hexapep_transf.
PROSITE; PG00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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15. TISSUE=Whole embryo;

15. TISSUE=Whole embryo;

16. TISSUE=Whole embryo;

17. Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,

18. Anamoto J., Wakamatsu A., Nagai T., Nakamura Y.,

18. Saito K., Yamamoto J., Rogai T.;

18. Saito K., Sugano S., Isogai T.;

18. Saito K., Sugano S., Isogai T.;

18. Sibmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

18. RBL; Ak075449; BAC11651.1;

18. GO: GO: GO: GOSTOB; C: extracellular matrix, IEA.

19. GO: GO: GOSTOB; F: extracellular matrix structural constituent; IEA.

19. ROG: GO: GOSTOB; F: extracellular matrix structural constituent; IEA.

19. RITEPRO: IPRO01451; Hexapep_transf.

19. RINTS; PRO1509; TROPOELASTIN.

19. PROSITE; PRO01101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                               MEDINE=96411691; PubMed=8812460; Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J., Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J., Koop H.H.O., Costa T., Pober B., Lew L., Brinkman J., Rommens J., Koop B.F., Tsui L.-C.; and the strong B.F., Tsui L.-C.; and the strong B.F., Tsui L.-C.; and the strong a S00-kb region at 7q11.23 that is commonly deleted in Williams syndrome patients."; Genomics 36:328-336(1996).
                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                      Last sequence update)
                                                                 258 AA.
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Homo sapiens (Human).
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last amnotation update)
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CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
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BMBL, ARIJ231; BAGS5506.1;
InterPro; IPR001451; Hexapep_transf.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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100.0%; Score 59; DB 2; Length 472; 100.0%; Pred. No. 0.14;
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                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 570 AA; 48941 WW; 3117B028D06D4F7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                        0;
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                                                                        0; Mismatches
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Homo sapiens (Human).
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Last sequence update) Last annotation update)

Created)

27, 27, 27, 27,

658 AA

PRT;

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhar N.K.,

Rah Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hesteh F.,

Brapleron M., Soares M.B., Bonaldo M.F., Casrvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carrinci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broker S.M., McKernan R.J., Maramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
                       PRELIMINARY;
                                           AAH65566;
02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                               (Human)
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Q14235
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Raugher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,
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Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                    0; Indels
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK122731; BAC85506.1; -3
SEQUENCE 570 AA; 48991 MW; 3117B028D06D4F7B CRC64;
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PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 658 AA; 56680 WW; SDAFCO0D16A2F94E CRC64;
                                                                                                                                                        Length
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                  ; Score 59; DB 2;
; Pred. No. 0.17;
0; Mismatches 0
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InterPro, IPR003979; tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                        100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                  450 ALAAAKAAKYGAA 462
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                                                                                                                                                                                                                                                                                   1 ALAAAKAAKYGAA 13
                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
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Best Local Similarity
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                                                 Gaps
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Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                    ;
100.0%; Score 59; DB 2; Length 658; 100.0%; Pred. No. 0.19;
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            687 AA.
                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                            PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                       538 ALAAKKAKKGAA 550
                                                                                                      1 ALAAAKAAKYGAA 13
                                                       Conservative
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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RESULT 6

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SEQUENCE FROM N.A.

TISSUE-Human fetal kidney;

POUSTKA A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX537939; CAD97910.1;

InterPro; IPR001451; Hexapep transf.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin fibroblast;

MEDLINE=89009960; PubMed=3171221;

REDLINE=8009960; DubMed=3171221;

Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,

Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;

"Cloning of full-length elastin DDNAs from a human skin fibroblast

recombinant cDNA library: further elucidation of alternative splicing

utilizing exon-specific oligonucleotides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM B).
MEDLINES #87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 2; Length 711; 100.0%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61765 MW; 95B624A99B4A989B CRC64;
                                                                                                                                                                    ELS_HUMAN STANDARD; PRT; 730 AA. P15502; 014233; 014238; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 01-APR-1990 (Rel. 44, Last annotation update) Elastin precursor (Tropoelastin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invest. Dermatol. 91:458-464(1988).
                                                                                                                                                     Created)
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=88156138; PubMed=2831431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25,
591 ALAAKKAAKYGAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 711 AA; 6:
                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                               Q7Z3F5;
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                                                                           RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO, GO:0030023; F:extracellular matrix constituent conferring. . .; NAS. InterPro; IPR001451; Hexapep_transf. InterPro; IPR003379; tropoelastin. InterPro; PR0150; TROPOELASTIN. PRINTS; PR01500; TROPOELASTIN. PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1. SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F_CRC64;
                 [2]
SEQUENCE FROM N.A.
MEDILINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
Rosenbloom J., Ornstein-Goldstein N.;
"Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";
of Alu resue Res. 16:197-211(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Human rectum tumor;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hauber W., Wieman S.;
Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538199; CAD98065.1; -.
InterPro; IPR001451; Hexapep transf.
PROSITE; PS00101; HEXAPEP_TRĀNSFERASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687 AA; 59847 MW; 79232A191DC1F10F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686021208 (Fragment).
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Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005578; C:extracellular matrix; NAS.
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M17279; AAC98393.1; JOINED.
M17281; AAC98393.1; JOINED.
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Best Local Similarity 100...
These 13; Conservative
                                                                                                                                                                                                   M17265; AAC98393.1;
M17266; AAC98393.1;
M17267; AAC98393.1;
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                                                                                                                                                                                                                                                                                            M17272; AAC98393.1;
M17273; AAC98393.1;
M17275; AAC98393.1;
                                                                                                                                                                                                                                                         M17268; AAC98393.1;
M17271; AAC98393.1;
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EMBL; M17282; AAC98394.1; -.
EMBL; M16983; AAC98394.1; JOINED.
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      ibroblasts."
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Similarity
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M17272;
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M17276;
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EMBL; M36860;
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Q14234
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SOTT FITTER WAS DRAWNERS OF THE FITTER OF TH
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Isold=P15502-2; Sequence=VSP 004243;

Isold=P15502-2; Sequence=VSP 004243;

Isold=P18EASE: Defects in ELN are a cause of autosomal dominant cutis

laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis.

-!- DISEASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:94050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.

-!- DISEASE: Defects in ELN are the cause of Supravalvular aortic stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal constant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thurscan T. Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P., Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;

"Isolated supraval-vular aortic stenosis: functional haploinsufficiency of the elastin gene as a result of nonsense-mediated decay.";

Hum. Genet. 106:577-588(2000).

-!-FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-!-SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-!-SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
                                                                                                                                                                                                                                                                                                                                        Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J., Keating M.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVOLVEMENT IN CUTIS LAXA.

MEDITNE=99091639; PubMed=9873040;

Shang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;

"Cutis laxa arising from frameshift mutations in exon 30 of the
                          Rosenbloom J., Uitto J.;
"Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LIM-Kinsel hemizygosity implicated in impaired visuospatial constructive cognition."; Cell 86:59-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elastin gene (ELN).";
J. Biol. Chem. 274:981-986(1999).
                                                                                                                                                                            Lab. Invest. 58:270-277(1988)
                                                                                                                                                                                                                                                            SEQUENCE OF 603-730 FROM N.A.
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Gaps
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GO; GO:0005518; C:extracellular space; TAS.
GO; GO:0005515; C:extracellular matrix structural constituent; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:0009887; P:crganogenesis; TAS.
GO; GO:0009887; P:respiratory gaseous exchange; TAS.
InterPro; IPR00379; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Allernative splicing; Connective tissue; Repeat; Signal;
Structural protein; Williams-Beuren syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Missing (in isoform 2).
/FTId=VSP 004243.
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Last annotation update)
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; AAC98394.1; JOINED.
; AAC98394.1; JOINED.
; AAA52382.1; -.
JOINED.
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                                                                        AAC98394.1; JOINED.
AAC98394.1; JOINED.
AAC98394.1; JOINED.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
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                                     AAC98394.1;
AAC98394.1;
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725
477
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HSSP; P50099; 1ZFJ.
Genew; HGNC:3327; ELN.
MIM; 130160; -.
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Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
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                                                                                                   "The DNA sequence of human Nature 424:157-164 (2003).
                                                                                                                                                                                                                                                                                                                                                                                      1 ALAAAKAAKYGAA 13
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02-MAR-2004 (
02-MAR-2004 (
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AAS07435;
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MEDLINE=22737999; PubMed=12853948;

Hiller L.W.; Fulton R.S.; Fulton L.A., Graves T.A., Pepin K.H.,

Magner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,

Magner-McPherson C., Layman D., Maso W.B.;

Mylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

Reali G.A., Delehaunty K.D., Miner T.L., Nash W.B.;

Mylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

Ros Sun H., Edwards J., Bardshaw-Cordum H., Ali J., Andrews S., Isak A.,

Nan H., Edwards J., Bardshaw-Cordum H., Ali J., Andrews S., Isak A.,

Nan H., Bdwards J., Scott K., Holmes A., Harkins R., Harris A.,

Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,

Latreille P., Miller M., Johnson D., Murray J., Woessner J.P.,

Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,

Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
                                                                                                                                                                                                                                                                                                                                            GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
                     SEQUENCE FROM N.A.
MEDLINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D. Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
"Structure of the 3' region of the human elastin gene: great abundance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.21;
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                                                                                   nences and few coding sequences.";
16:197-211(1987).
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01500; TROPOELÀSTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 757 AA; 66136 MW; 23B7FESBBAF8SCA8 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987)
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InterPro; IPR003979; tropoelastin.
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M17278; AAC98395.1; JOINED.
M17279; AAC98395.1; JOINED.
M17280; AAC98395.1; JOINED.
M17281; AAC98395.1; JOINED.
                                                                                                                                                                                                                                         M17274; AAC98395.1; JOINED.
M17275; AAC98395.1; JOINED.
M17276; AAC98395.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                   of Alu repetitive sequences
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EMBL; M17282; AAC98395.1;
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M17268; AAC98395.1;
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RAY SHOWNLE, FROW N.A.

RAY SHOUNCE, FROW N.A.

RAY MEDLINE-2737999; PubMed=12853948;

RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,

RA Wajner-McDherson C., Layman D., Mass J., Gager S., Walker R.,

RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

RA Wylie K., Schlon M., Decker M.C., O'Laughlin M.D., Schaller M.E.,

RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,

RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,

RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

RA Tih-Wollam A.M., Johnson D., Murray J., Woessner J.E.,

RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.E.,

RA Hickenborham M.T., Elared J., Walliams D., Bedell J.A., Mardis E.R.,

RA Hickenborham M.T., Elared J., Walliams D., Bedell J.A., Mardis E.R.,

RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,

RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,

RA Bady S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,

RA Raderston R.H., Wilson R.K.;
Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E., Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K., Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S., Baertsch R.A., Barth M.R., Kaibler E., Flicek P., Bork P., Suyama M., Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R., Eddy S.R., MoPherson J.D., Olson M.V., Bichler B.E., Green B.D., Waterston R.H., Wilson R.K.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.21;
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EMBL; AC005056; AAS07435.1; -
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSTTE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 757 AA; 66106 MW; 2B24F955DB360738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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MEDLINE=97358574; PubMed=9215670;

MEDLINE=97358574; PubMed=9215670;

MIDLINE=97358574; PubMed=9215670;

MIDLINE=97358574; PubMed=9215670;

Morris C.A., Keating M.T.;

"Elastin point mutations cause an obstructive vascular disease,
"I supravalvular aortic stenosis.";

Hum. Mol. Genet. 6:1021-1028(1997).

EMBL; U93037; AAB65620.1;

EMBL; U93034; AAB65620.1;

MR EMBL; U93035; AAB65620.1;

MR EMBL; U93035; AAB65620.1;

MR CO; GO:0005578; C:extracellular matrix; IEA.

RO; GO:0005578; C:extracellular matrix structural constituent; IEA.

RICHEPPO; IPR003979; tropoelastin.

RICHEPPO; PR0130979; tropoelastin.

PRINTS; PR01500; TROPOELASTIN.
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stemosis, Williams-Beuren syndrome)
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                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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les 12; Conservative
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EMBL, RAI25511, BAC861801; -
InterPro; IPR00399; tropoclastin.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                        Wilson R.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AC005056; AAS07435.1; -. Hypothetical protein. SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
                                     SEQUENCE FROM N.A.

Du H., Rohlfing T., Strong C.;

The sequence of Homo sapiens BAC clone CTB-51J22.";

Submitted (UNN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Waterston R.H.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43523.
Homo sapiens (Human).
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02-MAR-2004 (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 13; Conservative
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nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
     Nature 424:157-164(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                   Submitted (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        [5]
SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                      Waterston R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC86188
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ID BAC8
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AMEDINE-97358574; PubMed-9215670;
AMEDINE-97358574; PubMed-9215670;
AMEDINE-97358574; PubMed-9215670;
AMOTTIS C.A., Keating M.T.;
MOTTIS C.A., Keating M.T.;
Telastin point mutations cause an obstructive vascular disease,
AMEDINAL AMEDICAL STREAMS TOTAL STREAMS TANDER STREAMS TOTAL STREAMS TOTAL STREAMS TRANSFERASES; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
OLA T. Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P50099; 12FJ.

GO; GO:0005578; C:extracellular matrix; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR001451; Hexapep_transf.

InterPro; IPR003979; tropoelastin.
                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.5%; Score 54; DB 2; Length 635; Best Local Similarity 92.3%; Pred. No. 1.2; Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1500; TROPOBLASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 643 AA; 55629 WW; FDFC042617E72A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55279 MW; 72950C364127B2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBNB14;
QBNB14;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0254.
                                                                                     Last sequence update)
Last annotation update)
                                   635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 AA
                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK075554; BAC11696.1; -. HSSP; P50099; 1ZFJ.
                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AAAAKAAKYGAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALAAAKAAKYGAA 13
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                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635
                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 635 AA;
                                                                                                                         Elastin (Fragment)
                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                         Homo sapiens
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                                   015336
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Matches
RESULT 17
015336
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Genomics 23:125-131(1994).

-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- PTM: The crosslinks are made of deaminated Lys.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN=BALB/C; TISSUB=Lung;
MEDLINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090,
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
  Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 2; Length 810;
Pred. No. 2.2;
                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green B.D.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER 1 1 SEQUENCE 810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                       810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860 AA
                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
     Score 54;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Last annot
Elastin precursor (Tropoelastin)
91.5%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                         271 AAAAKAAKYGAA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 AKAAAKAAKYGAA 325
                                                                                                                   1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALAAAKAAKYGAA 13
  Query Match 91.5
Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELN (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
ELS_MOUSE
ID ELS_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Eln;
                                                                                                                                                                                                                                                                                                                                                  09ESZ9;
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                                                                                                                                                                                                                                                                                                                       Q9ESZ9
                                                                                                                                                                                                                                                                  RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/63; TISSUE=Thymus;
The FANTOW Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630042119 product:elastin, full insert sequence (Elastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                            89.8%; Score 53; DB 1; Length 860; 92.3%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                        Connective tissue; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     860 AA.
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                              Potential.
                                                                                                                                                                                                                                                            Elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-Thymus;
MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Thymus; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                        tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                   MGD; MGI:95317; Eln.
InterPro; IPR003979; tropoelae
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                          71955 MW;
                                                                                                                                     EMBL; U08210; AAA80155.1; -.
                                                                                                                                                                                                                                                                                                                                            92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                             363 AKAAKKAAKYGAA 375
                                                                                                                                                                                                                                                                                                                                                                                               1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001)
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                                                                                                                                                                                                                                                            860
                                                                                                                                                                                                                                                                            855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                              860 AA;
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                        PIR; A55721; EAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            850
                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
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STRAIN=FVBN'N; TISSUE=Mammary tumor. C3;

MEDLINE=22388257; PubMed=1247932;

MEDLINE=22388257; PubMed=1247932;

MAL Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Laschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Laschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brans S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley R.J., McErnan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergere B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=CSTBL/63; TISSUE=Thymus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Ishii Y., Itoh M., Kagawa T., Kaukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Komo H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murama M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Soqabe Y., Taqami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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თ
                                                                                 MEDLINE=20530913; PLOBMEG=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Hatsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabliwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika B., Matamatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rishika Gequence analysis (RISA) system-184-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bono H., Carninci P.,
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GO; GO:0007519; P:myogenesis; IMP.
GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
GO; GO:0043149; P:stress fiber formation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AK041860; BAC31084.1; -. EMBL; BC051649; AAH51649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7C340F2FFDC92E5 CRC64;
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PR01500; TROPOELASTIN.
Genome Res. 10:1617-1630(2000)
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MEDLINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
NRat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507 (1988)
-!-FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!-SUBNIT: The Polymeric elastin chains are cross-linked together into an extensible 3D network.
-!-SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!-ALTERNAȚIVE PRODUCTS:
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=92241859; PubMed=1572637; Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.; Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.; Flements of the rat tropealastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Franzblau C., Pratt C.A., Faris B., Colannino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.; "Role of tropoelastin fragmentation in elastogenesis in rat smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=8; Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
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Isold=099372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                     Rich C.B., Foster J.A.;
"Characterization of rat heart tropoelastin.";
Arch. Biochem. Biophys. 268:551-558(1989).
                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                          864 AA
                                                                                                                                           05-JUL-2004 (Rel. 44, Last annotation updat
Elastin precursor (Tropoelastin) (Fragment)
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                                                                                        PRT;
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                       363 AKAAKKAAKYGAA 375
                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 12:651-658(1992).
13
                                                                                         STANDARD;
                                                                                                                                                                                 Rattus norvegicus (Rat)
1 ALAAAKAAKYGAA
                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2768256;
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/rinc.vsr_04246.
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Missing (in isoform 2, isoform 5, isoform
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                                   004245, VSP_004246;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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MEDLINE=85280426; PubMed=2992576;

Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,

Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;

"Structure of the 3' portion of the bovine elastin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (In isoform 3, isoform
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PRINTS; PR01500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
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IsoId=Q99372-7; Sequence=VSP 004244, VSP 004246;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBELL; NCBI gi: 163003 (Fragment).
                                   IsoId=Q99372-8; Sequence=VSP 004244, VSP 0042
PTM: The crosslinks are made of deaminated Lys.
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EMBL, M86371, AAA42271.1, JOINED.
EMBL, M86376, AAA42272.1, -.
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EMBL; M86375; AAA42272.1; JOINED.
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MEDLINE=8802842; PubMed=3665402;
MEDLINE=8802842; PubMed=3665402;
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                              MEDLINE=88028442; PubMed=3665402; Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson Yeh H., Ornstein-Goldstein N., Tox IK., Rosenbloom J.; Rosenbloom J.; Sequence variation of bovine elastin mRNA due to alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%; Score 50; DB 2; Length 650; 84.6%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBEL3; NCBI gi: 163005 (Fragment).
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                                                                                                                                                                EMBL; M19372; AAA30499.1; CINED. BMBL; M19422; AAA30499.1; CINED. BMBL; M19366; AAA30499.1; CINED. BMBL; M19366; AAA30499.1; CINED. BMBL; M19366; AAA30499.1; CINED. BMBL; M19370; AAA30499.1; CINED. BMBL; M19370; AAA30499.1; CINED. BMBL; M22771; AAA30499.1; CINED. BMBL; M22771; AAA30499.1; CINED. BMBL; M22773; AAA30499.1; CINED. BMBL; M22774; AAA30499.1; CINED. BMBL; M22079; AAA30499.1; CINED. BMBL; M22079; AAA30499.1; CINED. BMBL; M2070; AAA30499.1; CINED. BMBL; M2010; AAA30499.1; CINED. BMBL; M2010; AAA30499.1; CINED.
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PRINTS; PR01500; TROPOELASTIN.
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MEDLINE=85280426; PubMed=2992576;
Biochemistry 24:3075-3080(1985)
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Matches 11; Conserv
                      [2]
SEQUENCE FROM N.A.
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NCBI_TaxID=9913;
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028096
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Gaps
EMBL; M19370; AAA30501.1; JOINED.
EMBL; M19371; AAA30501.1; JOINED.
EMBL; M22771; AAA30501.1; JOINED.
EMBL; M22772; AAA30501.1; JOINED.
EMBL; M22772; AAA30501.1; JOINED.
EMBL; M22774; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
EMBL; M22988; AAA30501.1; JOINED.
GQ; GG:0005201; F:extracellular matrix; IEA.
GQ; GG:0005201; F:extracellular matrix structural constituent; IEA.
INTERPO; IPR003979; LTOPOELASTIN.
PRINTS; PR01500; TROPOELASTIN.
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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MEDLINE=85280426; PubWed=2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.7%; Score 50; DB 2; Length 666;
84.6%; Pred. No. 6.1;
.ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 AA; 57652 MW; EB3C019E3BD7618D CRC64;
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Last sequence update)
Last annotation update)
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EMBL; M19422; AAA305001; 7.
EMBL; M19422; AAA305001; 7.
EMBL; M19466; AAA305001; 70INED.
EMBL; M19367; AAA305001; 70INED.
EMBL; M19369; AAA305001; 70INED.
EMBL; M19370; AAA305001; 70INED.
EMBL; M19370; AAA305001; 70INED.
EMBL; M19370; AAA305001; 70INED.
EMBL; M22771; AAA305001; 70INED.
EMBL; M22771; AAA305001; 70INED.
EMBL; M22774; AAA305001; 70INED.
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PRINTS; PR01509; TROPOELASTIN.
NON_TER
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Length 679;

Score 50; DB 2;

us-09-743-818a-13.rup

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05-JUL-2004 (Rel.
Elastin precursor
                                                                                                                                                                            Bovinae; Bos.
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                                                            Name=ELN;
   NAME NO DESCRIPTION OF THE PROPERTY OF THE PRO
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                              Indels
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                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Elastin; NCBI gi: 163002 (Fragment).
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                                                                                                                                                                                                                                                                                             707 AA.
ed. No. 6.2;
Mismatches
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EMEL, M19422; AAA30498.1; -
EMEL, M19422; AAA30498.1; -
EMEL, M19366; AAA30498.1; JOINED.
EMEL, M19366; AAA30498.1; JOINED.
EMEL, M19369; AAA30498.1; JOINED.
EMEL, M19369; AAA30498.1; JOINED.
EMEL, M19370; AAA30498.1; JOINED.
EMEL, M19370; AAA30498.1; JOINED.
EMEL, M19371; AAA30498.1; JOINED.
EMEL, M22771; AAA30498.1; JOINED.
EMEL, M22771; AAA30498.1; JOINED.
                                                                                                                                                                                                                                                                                             PRT;
   Pred.
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PRINTS; PR01500; TROPOELASTIN.
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M22774; AAA30498.1; JOINED.
M22775; AAA30498.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M22988; AAA30498.1; JOINED M23010; AAA30498.1; JOINED
84.6%;
                                                                                                                                              264 AAAAKAAKFGAA 276
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                                                                                        1 ALAAAKAAKYGAA 13
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Local Similarity 84.6
nes 11; Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing."
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EMBL;
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Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
Brown an intrachain disulfide bond that stabilizes a loop structure and positively charged pocket.";
Blochem Biophys. Res. Commun. 186:549-555(1992).
-!-FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!-SUBUNT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
-!-SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the bovine elastin gene and SI nuclease analysis of alternative splicing of elastin mRNA in the bovine nuchal ligament."; Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-27 FROM N.A. MEDIINE=91234332; PubMed=2031719; Manchar A., Shi W., Anwar R.A.; Marchar characterization of bovine elastin gene; comparison with the gene for human elastin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raju K., Anwar R.A.;
Prinary structures of bovine elastin a, b, and c deduced from the
"exquences of cDNA clones";
J. Biol. Chem. 262:5755-5762(1987).
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01500; TROPOBLASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=3; Synonyms=C;
IsoId=P04985-3; Sequence=VSP 004240;
-!- PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
44, Last annotation update) (Tropoelastin).
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IsoId=P04985-2; Sequence=VSP_004239;
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IsoId=P04985-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Cell Biol. 69:185-192(1991).
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EMBL; K03506; AAA30506.1; -.
EMBL; J02855; AAA30776.1; -.
EMBL; M58652; AAA3519.2; -.
PIK; A31865; EABO.
InterPro; IPR003979; tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Nuchal ligament;
MEDLINE=89274159; PubMed=2543440;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87194772; PubMed=3032943;
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                                                                                                                      Bos taurus (Bovine).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=87242330; PubMed=3593675;
Bressan G.M., Argos P., Stanley K.K.;
"Repeating structure of chick tropoelastin revealed by complementary DNA cloning.";
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0
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/FTIGAVSP_004239.
Missing (in isoform 3).
/FTIGAVSP_004240.
MRS - MAG (in Ref. 2 and 3).
E - S (in Ref. 2 and 3).
%; 633C03E411643D83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 1; Length 747;
Pred. No. 6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION STREET, 190 AN., 190 AN., 190 AN., 190 AN., 191 AUG-1988 (Rel. 08, Created) 191 AUG-1988 (Rel. 04, Last sequence update) 191 August annotation update) Blastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                          Allysine.
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Missing (
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                                                     Allysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Aorta;
MEDLINE=87297534; PubMed=3502711;
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84.6%;
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RESULT 28
ELS_CHICK
ID _ ELS_CHICK
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                                   Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.; "Sequence analysis of elastin cDNA from chick aorta and tissuespecific transcription of the elastin gene in developing chick
                                                                                                                                                                                                                                                                                                                                                                      EMBL; W21880; AAA49082.1; -.
EMBL; M15889; AAA49108.1; -.
PIR; A26601, A26601. Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR003979; tropoelastin.
Pfam; PF01391; Collagen. 1.
PRINTS; PR0130; TR00ELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                Name=2; Synonyms=Embryonic;
IsoId=P07916-2; Sequence=VSP 004241, VSP 004242;
-!- PTM: The crosslinks are made of deaminated Lys.
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By similarity.
Allysine (Potential).
Allysine (Potential).
                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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8 X tandem repeats.
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IsoId=P07916-1; Sequence=Displayed;
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NON TER 1
SIGNAL <1
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(Potential)

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Search completed: November 19, 2004, 16:36:44 Job time: 7.62838 secs
  Elastin (Tropoelastin) (Fragment).
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Allysine (Potential).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                                                                                                                                                                                                                                                                                                                                                                                           'Blastin: relation of protein and gene structure to disease.";
                                                                                                                                                              DB 1; Length 750;
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                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                         69 AA.
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                                                                                                                                                             84.7%; Score 50; DB: 91.7%; Pred. No. 6.7;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   Lab. Invest. 51:605-623(1984).

EMBL; M31899; AAA6417.1; -

EMBL; M31894; AAA96417.1; JOINED.

EMBL; M31895; AAA96417.1; JOINED.

EMBL; M31896; AAA96417.1; JOINED.

EMBL; M31897; AAA96417.1; JOINED.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Les 10; Conservative
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750 AA;
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                                                                                                                                                                      Best Local Similarity
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NCBI_TaxID=9913;
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P11547;
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                                                                                                                                                                                                                                                                                                                                                     *Analysis of the 3' region of the sheep elastin gene.";
Arch. Biochem. Biophys. 241:684-691(1985).
-!-PUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completel-into an extensible 3D network.
-!-SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
-!-SUBCELULIAR LOCATION: Extracellular matrix of elastic fibers.
-!- PTM: The crosslinks are made of deaminated Lys.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
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Yoon K., Davidson J.M., Boyd C., May M., Luvalle P.,
Ornstein-Goldstein N., Smith J., Indik Z., Ross A., Golub E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1; Length 100; Pred. No. 4;
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5C680C6A5AEE6786 CRC64;
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EMBL; M26189; AAA31516.1; -.
PIR; S59623; S59623.
Connective tissue; Repeat; Structural protein.
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                                                                                                                                   NCBI_TaxID=9940;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 19, 2004, 16:37:11 Run on:

.; Search time 84.1092 Seconds (without alignments) 2168.321 Million cell updates/sec

Title: Perfect score:

US-09-743-818A-71 2680 1 GGVPGAIPGGVPGGVFYPGA......GGVAAAAKSAAKVAAKAQLR 515 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1570615 seqs, 354127592 residues

1570615

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Listing first 100 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

			Description	Sequence 1, Appli	Sequence 38, Appl	Sequence 8, Appli	Sequence 40, Appl	Sequence 2477, Ap	Sequence 2915, Ap	Sequence 38, Appl	Sequence 38, Appl	Sequence 28, Appl	Sequence 27, Appl	Sequence 31, Appl	Sequence 26, Appl	Sequence 29, Appl
SUMMARIES			ΠD		US-10-210-172-38	US-09-961-403-8	US-10-210-172-40	US-10-108-260A-2477	US-10-104-047-2915	US-09-837-969A-38	US-09-841-321A-38	US-08-806-029-28	US-08-806-029-27	US-10-800-179-31	US-08-806-029-26	US-08-806-029-29
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Sequence 19, Appl Sequence 10, Appl Sequence 61, Appl Sequence 53, Appl Sequence 68, Appl Sequence 69, Appli Sequence 64, Appl Sequence 51, Appl Sequence 51, Appl Sequence 31, Appl Sequence 31, Appl Sequence 7032, Appl Sequence 16, Appl Sequence 16, Appl	). DOMENT LIMITED PARTNERSHIP PEPTIDES MODELED ON HUMAN ELASTIN AND PROTEINS 964,662	Indels 0; Gaps 0;   GGLACGGLACGAEPAVT 60   GGLACGGLACGAEPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAPAVT 60   GGLACGAEGAEGAEGAEGAEGAEGAEGAEGAEGAEGAEGAEGAEG
17 US-10-479-638-49 9 US-09-861-597-10 16 US-10-720-025-61 17 US-10-479-638-53 14 US-10-342-331-4 16 US-10-70-025-58 8 US-08-806-029-9 14 US-10-096-986-64 16 US-10-720-025-51 17 US-10-479-638-21 14 US-10-36-493-7032 17 US-10-479-638-16 15 US-10-479-638-16 15 US-10-479-638-16	1111 LITI EVEI ING ROUS 09 / 09 / 70 / 70 / 70 / 70 / 70 / 70 /	9.6\$;   Score 2670;   DB 10;   Length 731;     9.6\$;   Pred. No. 6.1e-139;     0.6   Mismatches   2;   Indels   0;   Gaps     0.7   Mismatches   2;   Indels   0;   Gaps     0.8   Mismatches   2;   Indels   0;   Gaps     0.8   Mismatches   2;   Indels   0;   Gaps     0.9   Mismatches   2;   Indels   1;   Ind
20.5 1128 20.1 714 19.8 1314 19.6 720 19.5 1830 19.4 1177 19.3 821 19.3 520 19.0 1759 18.7 780	Application US/No. US200301666 No. US200301666 DRMATION: PROTEIN SPECIAL HSC RESEARCH AVENTION: SELF-7 NVENTION: OTHER SANCE: 041082/011 PLICATION NUMBER: LING DATE: 200 LING DATE: 1999-06 SEQ ID NOS: 11 Patentin Ver. 2 31 Homo sapiens	PGGVPC PGGVPC PGGVPC PGGVPC PGGVPC PGGVADA VLPGAR VLPGAR PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGVGC PGGV PGGV
87 550 88 539.5 89 531.5 90 524 91 524 93 519 94 519 96 516 97 514.5 98 509 99 501.5	RESULT 1 US-09-964-662-1 US-09-964-662-1 Sequence 1, Application US/0996 Publication No. US2030166846A1 GENERAL INFORMATION: APPLICANT: PROTEIN SPECIALTIES APPLICANT: HOROTEIN SELF-ALIGN TITLE OF INVENTION: OTHER FIB TITLE OF INVENTION: OTHER FIB TITLE FEFENCE: 041082/0112; CURRENT FILLING DATE: 12909-06 SURRENT FILLING DATE: 1299-06 SOUTHARE OF SEQ ID NOS: 11 SOUTHARE: PATENTIAN OFF. 1299-06 TITLE OF SEQ ID NOS: 11 SEQ ID NO 1 LEMOTH: 731 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT	Ouery Match Beet Local Similarii Batches 513; Conse Oy 1 GGVPGAII Db 1 GGVPGAII OY 61 FPGALVP OY 121 PGVYPGG OY 301 PGFGPGV OY

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 19, 2004, 16:06:25; Search time 23.1638 Seconds (without alignments) 2139.188 Million cell updates/sec Run on:

US-09-743-818A-71 2680 1 GGVPGAIPGGVFYPGA......GGVAAAAKSAAKVAAKAQLR 515 Title: Perfect score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 100 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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R;Yoon, K.; Davidson, J. M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.;
Arch. Biochem. Biophys. 241, 684-691, 1985
A;Title: Analysis of the 3' region of the sheep elastin gene.
A;Reference number: A24758; MUID:85305763; PMID:3839997
A;Accession: A24758; MUID:85305763; PMID:3839997
A;Accession: A24758
A;Molecule type: MRNA
A;Residues: 655-669,671-716,732-770 <YOO>
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;760-765/Disulfide bonds: #status predicted
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PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKF 266
                                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                                                                                   AKAAKŸGAAGAGVLGGLVPGPQAAVPGVPGTGGVPGVĞTPAAAAAKAAAKAAĞFALLNLA 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tropolastin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59623; A24758
R;Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; De
Matrix Biol. 14, 635-641, 1994
A;Title: Extensive alternate exon usage at the 5' end of the sheep tropoelas
A;Reference number: S59623
                                                                                                                                                                                                    PGFGPGVVGVPGAGVPGGGGTPVVPGAGTPGAAVPGVVSPEAAAKAAAKAAKYGAR
                                                    GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
                                                                                                         GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 GVKPGKVPGVGLPGVYPGGVLPGTGARFPGIGVLPGVPTGAGVKRARAPGGGRFAGIPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSA
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Nylleringle names: tropocalasting
Nylleringle names: tropocalasting
Clybecies: Homo sapiens (man)
Clybecies: Homo sapiens (man)
Clybecies: A37707, A37705, A30524, A5891
Clyccesion: A37707, A37705, A30524, A5891
Clyccesion: A37707, A37705, A30524, A5891
Clyccesion: A37707, A37705, A37705, A30524, A5891
Clyccesion: A37707, A37705, A37705, Mulb.8728968; PMID:3039501
A;Reference number: A37707, WUID:8728968; PMID:3039501
A;Reference number: A37707, WUID:8728968; PMID:3039501
A;Reference number: A37707, WUID:8728968; PMID:3039501
A;Residues: 1-500,507-792
A;Reference number: A33705
A;Reference number: A30524
A;Reference numbe
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A;Gene: GDB:ELN
A;Cross-references: GDB:119107; OMIM:130160
A;Map position: 7q:1.23-7q:1.23
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular
F;1-26/Domain: signal sequence #status predicter
F;7-792/Product: elastin #status predicted <MX
F;782-797/Disulfide bonds: #status predicted <MX
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
                                                OM protein - protein search, using sw model
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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ALIGNMENTS

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MEDINE-22737999; PubMed=12853948;

MEDINE-22737999; PubMed=12853948;

MEDINE-22737999; PubMed=12853948;

MAGNET-MCPHERSON C., Dayman D., Mass J., Jaeger S., Walker R.,

MAGNET-MCPHERSON C., Dayman D., Maner T.L., Nash W.E.,

RA, Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,

RA, Delehaunty K.D., Miner T.L., Nash W.E., Cardes M., Du H.,

RA, Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

Nanbrunt A., Ngiyen C., Du F., Lamar B., Courtney L., Kalicki J.,

RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,

RA, Marcon C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

RA, Marcille P., Miller M., Minx P., Maupin R., Strowmatt C.,

RA, Latreille P., Miller M., Johnson D., Murray J., Woessner J.P.,

Rendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,

RA, Hickenbotham M.T., Elered J., Walliams D., Bedell J.A., Mardis E.R.,

RA, Hickenbotham M.T., Elered J., Marra M., Raymond C., Haugen B.,

RA, Simms E., Levy R., Clendening J., Kaul R., Kent W.J., Furey T.S.,

RA Bailey J.A., Pernt M.R., Keibler E., Flicek P., Bork P., Suyama M.,

RA, Baddy S.R., McPherson J.D., Olson M.V., Eichler E.B., Green E.D.,

MARLESON R.H., Milson R.K., Richer R.K.,

RA, Baddy S.R., McPherson J.D., Olson M.V., Eichler E.B., Green E.D.,

MARLESON R.H., Milson R.K., Richer R.M., Millison R.K.,

RA, Materston R.H., Milson R.K., Sichler F.B., Green E.D.,

MARLESON R.H., Milson R.K., Richer R.M., Milson R.Y., R.M.,

MARLESON R.H., Milson R.K., Richer R.M., Green E.D.,

MARLESON R.M., Milson R.K., Richer R.M., Milson R.V., Mils
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267 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG 326
                                                                                                                                                                                                                    PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA 420
                                                                                                                                                                                                                                                 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGGVGVAPGVGLAPGGVGVAPG 480
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                                                             GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001451; Hexapep_transf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87274906; PubMed=3038460; MEDLINE=87274906; PubMed=3038460; Cicila G., Rosenbloom J., Indix Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J., Ornstein-Goldstein N.; "Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences."; Connect. Tissue Res. 16:197-211(1987). EMBL; M17282; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGVPGAIPGGVPGGVFYPGAGLGALGCGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                                                                                                                                                                                                                                                                              MEDLINE=87289668; PubMed=3039501; Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Rosenbloom J., Rosenbloom J., "Alternative splicing of human elastin mkNa indicated by sequence analysis of cloned genomic and complementary DNA."; Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL; M17280; AAC98395.1; JOINED.
EMBL; M17281; AAC98395.1; JOINED.
GO, GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030023; F:extracellular matrix constituent conferring.
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SEQUENCE 757 AA; 66136 MW; 23B7FE5B8AF85CA8 CRC64;
                                                                                                                                Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.3e-99;
live 0; Mismatches 0;
                                                                      757 AA
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InterPro; IPR003979; tropoelastin.
                                                                                                               Created)
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M.7270; AAC98395.1; JOINED.
M.7271; AAC98395.1; JOINED.
M.7272; AAC98395.1; JOINED.
M.7273; AAC98395.1; JOINED.
M.7274; AAC98395.1; JOINED.
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EMBL; M17277; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M17265; AAC98395.1; JOINED.
M17266; AAC98395.1; JOINED.
M17267; AAC98395.1; JOINED.
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Best Local Similarity 100.
Matches 515; Conservative
                                                                        PRELIMINARY;
                                                                                                             (TrEMBLrel.
                                                                                                                                01-NOV-1996 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                               01-NOV-1996
01-NOV-1996
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Wilson R.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                    PRINTS; PRO1500; TROPOELÁSTIN.
PROSTIE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
HYPOCHELOID protein.
SEQUENCE 757 AA; 66106 MW; 2824F955D8360738 CRC64;
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02-MAR-2004 (TEMBLEEL: 27,
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120 180 146 240 266 326 360 386 300 420 446 480 506 98 9 Latreille P., Miller N., Johnson D., Murray J., Woessner J.P., Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J., Blein T.A., Nelson J.O., Berkowicz N., Wohldman P.E., Cook L.L., Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R., Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E., Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E., Simms E., Levy R., Clendenning J., Kaul R., Reth W.J., Furey T.S., Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M., Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R., Materston R.H., Wilson R.K., Materston R.H., Wilson R.K., Materston R.H., Wilson R.K., I., I. 27 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAFPAVT PIKAPKL.PGGYGL.PYTTGKL.PYGYGPGGVAGAAGKAGYPTGTGYGPQAAAAAAKAAAKF 447 AKAAKYGVGTPAAAAAKAAAKAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGG 1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPOPGAGVKPGKVPGVGL PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY 267 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGG PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAKAAAKAAKYGAR 421 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG 147 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKF 241 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAKYGAAAGLVPGG PGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKYGAR PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGGSPEAQAAAA Gaps . 0 757; 1; Indels Du H., Rohlfing T., Strong C.; "The sequence of Homo sapiens BAC clone CTB-51J22."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. Length the EMBL/GenBank/DDBJ databases to the EMBL/GenBank/DDBJ databases EMBL/GenBank/DDBJ databases Hypothetical protein. SEQUENCE 757 AA; 66106 MW; 2B24F955DB360738 CRC64; 99.9%; Score 2676; DB 2; 99.8%; Pred. No. 1.8e-99; iive 0; Mismatches 1; 515 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR

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PubMed=10942104;
Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
"Isolated supravalvular aortic stenosis: functional haploinsufficiency of the elastin gene as a result of nonsense-mediated decay.";
Hum. Genet. 106:577-588 (2000).
-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Skin fibroblast,
MEDLINE-89009960; PubMed=3171221;
Razlo M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
Crnstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
"Cloning of full-length elastin cDNAs from a human skin fibroblast
recombinant cDNA library: further elucidation of alternative splicing
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MEDLINE-96291399; PubMed-8689688;
Prangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green B.D.,
Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
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MEDLINE=99091639; PubMed=9873040;
ABDLINE=29091639; PubMed=9873040;
ABDLINE=209091639; PubMed=9873001, Tiller G.E., Davidson J.M.;
"Cutis laxa axising from frameshift mutations in exon 30 of the
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM B).
MEDLINES-87896668 PubMed=309501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.; Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88156138; PubMed=2831431; Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosenbloom J., Uitto J.; Fazio M.J. association and characterization of human elastin cDNAs, and ageassociated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keating M.T.;
"LIM-kinasel hemizygosity implicated in impaired visuospatial
             P15502; Q14233; Q14238;
01-ARE-1990 (Rel. 14, Created)
01-APE-1990 (Rel. 14, Last sequence update)
02-UUL-2004 (Rel. 44, Last annotation update)
730 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              utilizing exon-specific oligonucleotides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Invest. Dermatol. 91:458-464 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 274:981-986(1999).
                                                                                                  Elastin precursor (Tropoelastin)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lab. Invest. 58:270-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 603-730 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructive cognition.";
Cell 86:59-69(1996).
STANDARD;
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                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elastin qene (ELN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eibroblasts.";
ELS HUMAN
                                                                                                                          Name=ELN;
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Isold=P15502-2; Sequence=VSP 004243;
Isold=P15502-2; Sequence=VSP 004243;
-!- PFM: The crosslinks are made of deaminated Lys.
|-- D18EASB: Defects in ELN are a cause of autosomal dominant cutis laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric senosis.
|-- D15EASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.
|-- D15EASE: Defects in ELN are the cause of supravalvular aortic stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0005518; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
GO; GO:000818; P:cell proliferation; TAS.
GO; GO:000987; P:organogenesis; TAS.
GO; GO:000987; P:organogenesis; TAS.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TR0POELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                   isoId=P15502-1; Sequence=Displayed;
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AAA52382.1; -AAA53190.1; -AAA53190.1; -AAB17544.1; -AAB17544.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED
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EMBL; M16983; AAC98394.1; JC
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EMBL; M17266; AAC98394.1; JU
EMBL; M17267; AAC98394.1; JU
EMBL; M17269; AAC98394.1; JU
EMBL; M17270; AAC98394.1; JU
EMBL; M17270; AAC98394.1; JU
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AAC98394.1;
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AAC98394.1;
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HSSP; P50099; 12FJ.
Genew; HGNC:3327; ELN.
MIM; 130160; -.
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EMBL; M17273; P
EMBL; M17276; P
EMBL; M17276; P
EMBL; M17277; P
EMBL; M17279; P
EMBL; M17280; P
EMBL; M17280; P
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EMBL; M37881; P
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Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  FPGALVPGGVADAAAAXKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                             1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                              27 GGVPGAIPGGVPGGVFYPGAGLGALGGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                             9
                                                                          DB 1; Length 730;
                                                                                            Indels
                730 Elastin.
725 By similarity.
477 Missing (in isoform 2).
/FTIG=VSP 004243.
63260 MW, AB06D15BAS67AE46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BX537339, CAD97910.1, ...
InterPro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Hypochetical protein.
SEQUENCE 711 AA; 61765 MW; 958624A9984A989B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OM-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686F06102.
Name=DKFZp686F06102;
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                                                                         Score 2667; DB 1
Pred. No. 4e-99;
0; Mismatches
Williams-Beuren syndrome.
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98.8%;
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                  730
Structural protein;
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472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AAAKFGAGAAGVLPGVGGAGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAG
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001379; tropoelasin.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=97358574; PubMed=9215670;
Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
Morris C.A., Keating M.T.;
"Elastin point mutations cause an obstructive vascular disease,
            Length 711;
                                                         Indels
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Last annotation update)
            DB 2;
       Score 2659.5; DB 2;
Pred. No. 7.9e-99;
0; Mismatches 1;
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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EMBL; U93037; AAB65620.1; --
EMBL; U93034; AAB65620.1; JOINED.
EMBL; U93035; AAB65620.1; JOINED.
EMBL; U93035; AAB65620.1; JOINED.
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Query Match
Best Local Similarity 98.8
Matches 514; Conservative
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=97358574; PubMed=9215670;
Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
Morris C.A., Keating M.T.;
"Elastin point mutations cause an obstructive vascular disease,
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Pred. No. 1e-97;
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Hum. Mol. Genet. 6:1021-1028(1997).
EMBL; U93037; AAB65621.1; JOINED.
EMBL; U93034; AAB65621.1; JOINED.
EMBL; U93035; AAB65621.1; JOINED.
EMBL; U93036; AAB65621.1; JOINED.
GO; GO:0005578; C:extracellular matri
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
GO:0005201; F:extracellular matrix structural constituent; IEA.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Last annotation update)
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                       InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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Pred. No. 1e-97;
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Homo sapiens (Human)
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GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
                           MEDLINE=87274906; PubMed=3038460; MEDLINE=87274906; PubMed=3038460; Cicila G., Rosenbloom J., Charrow S.D., Cicila G., Rosenbloom J., Ornstein-Goldstein N.; "Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences."; Consect. Tissue Res. 16:197-211(1987).
                                                                                                                                                                                                                                                                                                                                                                                                             27 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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96.0%; Score 2571.5; DB 2; Length 687;
Best Local Similarity 96.3%; Pred. No. 2.5e-95;
Matches 496; Conservative 0; Mismatches 0; Indels 19;
                                                                                                                                                                                                                                                                                       InterPro; IPR001451; Hexapep transf.
InterPro; IPR001979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PR010101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 687 AA; 59529 WW; 864068C4C8E9F88F CRC64;
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 analysis of cloned genomic and complementary DNN
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 522
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                                                                                                                                                                                                                                                                                        TISSUE-Human rectum tumor;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo (Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538199; CAD98065.1;
InterPro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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Pred. No. 1.7e-92;
0; Mismatches 1
                                                                                                        Hypothetical protein DKFZp686021208 (Fragment)
Name=DKFZp686021208;
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les 485; Conservative
PRELIMINARY;
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468; Conservative
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                                                                                                                                                                                                           PRELIMINARY;
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02-MAR-2004
02-MAR-2004
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Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Riausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A picchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bronstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley R.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Catarrhini; Hominidae; Homo.
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Strauberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC06556; AAH65566.1; -.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Created)
Last sequence update)
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                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932;
                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Best Local Similarity 93.2
Matches 468; Conservative
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                                                                       Homo sapiens (Human)
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RA Strausberg R.L., Feingold E.A., Crouse L.H., Derge J.G.,
Rha Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rhad Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Rhad Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhard N.K.,
Rhad S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rhad S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rhad S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rhad S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rhad S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rhad S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rhad J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhadlesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rhadlesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Ry Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Ry T.Genration and initial analysis of more than 15,000 full-length human
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                                                                                                                                AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
                                                                                                                                                                  PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC065566, AAH65566.1, -. SDAPC00D16A2F94E CRC64; SEQUENCE 658 AA; 56680 MW; 5DAPC00D16A2F94E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 AA
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                                                                                                                                                                                                                                                                                                                          474 VGVAPGVGVAPGIGPGGVAGAA 495
                                                                                                                                                                                                                                                                          VGVAPGVGVAPGIGPGGVAAAA 502
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MEDLINE=22388257; PubMed=12477932;
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360
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                            231 GAGAAGVLPGVGGAGVPGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAAAAAGAAAGIVPGG
                                                                                                   291 PGFGPGVVGVPCAGVPGVGVPGAGIPVVPGAGIPGAAVFGVVSPEAAAKAAAKAAKYGAR
         GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
                                                                                                                                                                                                   --EAOAAA
                                                                                                                                                                                                                               421 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
                                                                                                                                                       PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FPGALVPGGVADAAAAKAAAKAGAGLGGVPGVGGLGVSA----GAVVPQPGAGVKPGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 FPGALIVPGGVADAAAAKAAAGAGLGGVPGVGGLGVSAAPSVPGAVVPQPGAGVKPGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arita M., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Tusashino K., Yuuki H., Hara H., Suqiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma I., Murakawa K., Kanehori K., Suqiyama A., Kawakami B., Suzuki Y., Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AK125511, BAC8618811. - InterPro; IPR003979; tropoelastin.

PRINTS; PR01500; TR0POELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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Pred. No. 1.4e-73;
0; Mismatches 1; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53787 MW; 20938FFEC5492A01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43523.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                    481 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                                                                                                                                           559
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96.0%;
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                                                                                                                                                                                                                                                                  385 AKAAKY-----
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TISSUE=Placenta;
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                                                                                                                                                       361
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                                                                      GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKYGAAAGLVPGG
                                                                                                       GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGG
PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKF
                                ------GYGPGGVAGAAGKAGYPTGTGVGPQAAAAAKF
                                                                                                                                                                                                                  PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGGSPEAQAAA
                                                                                                                                                                                                                                                                                           AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FPGALVPGGVADAAAAYKAAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Gaps
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001979; tropoelastin.
InterPro; IPR003979; tropoelastin.
PRINTS; PR015001; TR0POELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii Baito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y., Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AR075554; EAC11696.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2161.5; DB 2; Length 643;
Pred. No. 5e-79;
0; Mismatches 1; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Hypothetical protein PSEC0254.
Howo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKP-
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                                                                                                                                                                                                                                                                                                                                                                                                  VGVAPGVGVAPGIGPGGVAGAA 495
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Matches 433; Conservative
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                                    PIKAPKLP
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Msuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AKI25511; BAC8681881.; -.
SEQUENCE 559 AA; 53787 MW; 2093BFFEC5492A01 CRC64;
LVPGGPGFGPGVVGVPGAGVPGVGGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAA
                            02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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BAC86188;
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AR Tanigami A., Pujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
Ra Tanigami A., Pujiwara T., Sato H., Watanabe T., Ozaki K., Sugiyama T.,
Ra Irie R., Oteuki T., Sato H., Wakamatu A., Ishiis., Yamamoto J.,
Ra Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kiwuchi H., Kanda K.,
Ra Tisono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kiwuchi H., Kanda K.,
Ra Magtsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Ra Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Rabi K., Isogai T., Sugano S., Nagahari K.,
Rabi AK122731; BAC85506.1; ---
Rabi AK12731; RABI AK12731; RABI AK12731; RABI AK1317B028D06D4F7B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 570;
                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                             05-JUL-2004 (TrEMBLrel: 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 1.9e-67;
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PRT;
                                                                                                                                  Hypothetical protein FLJ16246.
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Matches 378; Conservative
PRELIMINARY;
                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Blastin precursor (Tropoelastin)
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              02-MAR-2004 (TYEMBLrel. 27, Created)
02-MAR-2004 (TYEMBLrel. 27, Last sequence update)
02-MAR-2004 (TYEMBLrel. 27, Last annotation update)
CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
                                                                                                                                                                                                                                  Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Wakanabe T., Ozaki K., Sugiyama T., Irie R., Oteuki T., Sato H., Wakanatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGYGPQAAAAAAAAKAAAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 GAGAAGVLPGVGGAGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAAAAAAAAGLVPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAA
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 570;
                                                                                                                                                                                                                                                                                                                                                                              Masuno Y., Nagai K., Isogai T., "NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AK122731, BAC85506.1, -. SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.8%; Score 1870; DB 2; 73.4%; Pred. No. 1.9e-67; ive 1; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.49
Matches 378, Conservative
                                                                                                                   sapiens (Human)
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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ELS. BOVIN STANDARD; PRT; 747 AA. P04585; P04986; P04987; C29421; 13-AUG-1987 (Rel. 05, Created) 3-AUG-1987 (Rel. 05, Last sequence update) 05-ULL-2004 (Rel. 44, Last annotation update)

SHERE

ELS BOVIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92337651; PubMed=1632791;
Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
"The cysteine residues in the carboxy terminal domain of tropoelastin form an intrachain disulfide bond that stabilizes a loop structure and positively charged pocket.";
Biocham Biophys. Res. Commun. 186:549-555(1992).
-I. FUNCTION: Major structural protein of tissues such as aorta and muchal ligament, which must expand rapidly and recover completely.
-I. SUBUNIT: The polymenic elastin chains are cross-linked together
                                                                                                                                                                                                                                                                                                   TISSUE-Nuchal ligament;
MEDLINE-89274159; PubMed=2543440;
Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
Rosenbioom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-27 FROM N.A.
MEDLINE=91234332; PubMed=2031719;
Manohar A., Shi W., Anwar R.A.;
"Partial characterization of bovine elastin gene; comparison with the
                                                                                                                                                                                                                                                                                                                                                                                   Rosenbloom J.;
"Structure of the bovine elastin gene and S1 nuclease analysis of allernative splicing of elastin mRNA in the bovine nuchal ligament."; Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                      Raju K., Anwar R.A., "Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones.";
                                                                        Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROISOO; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal; Structural protein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=3; Synonyms=C;
IsoId=P04985-3; Sequence=VSP 004240;
-!- PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=B;
IsoId=P04985-2; Sequence=VSP_004239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1; Synonyms=A;
IsoId=P04985-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene for human elastin.";
Biochem. Cell Biol. 69:185-192(1991)
                                                                                                                                                                                                                                                  Biol. Chem. 262:5755-5762(1987)
                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87194772; PubMed=3032943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003979; tropoelastin.
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EMBL, K03505; AAA30505.1; --
EMBL, K03506; AAA30506.1; --
EMBL, J02855; AAA30776.1; --
EMBL, M58652; AAA33776.1; --
EMBL; M58652; AAA33519.2; --
PIR, A31865; EABO.
                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-27 FROM N.A.
                                      Bos taurus (Bovine).
                                                                                                                NCBI_TaxID=9913;
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SO SET THE FET THE FET

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180 GKLPYGFGPGGVAGSAGKAGYPTGTGVGPQ-AAAAAAAAAKLGAGGAGVLPGVGVGGAG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GLGGVPGVGGLGVSAGAVVPQ----PGAGVKPGKVPGVGLPGVYPGGVLP--GARFPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
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Z
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88028442; PubMed=3665402;
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson Neh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson Rosenbloom J.C., Ciclia G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 679;
                                                                                                                                                                                                                                                                           S.
                                                                                                                                                                                                                                                              MEDLINE-85280426; PubMed-2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow
Th.H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679 AA; 57652 MW; EB3C019E3BD7618D CRC64;
                                                                                                                        01-NNV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Elastin-CBEL2; NCBI gi: 163004 (Fragment).
Bos taurus (Bovine).
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Pred. No. 5.8e-65;
                                                                                 679 AA
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                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWEL, M19369, AAA30500.1, JOINED.
EWEL, M19370, AAA30500.1, JOINED.
EWEL, M19371, AAA30500.1, JOINED.
EWEL, M22771, AAA30500.1, JOINED.
EWEL, M22772, AAA30500.1, JOINED.
EWEL, M22773, AAA30500.1, JOINED.
EWEL, M22774, AAA30500.1, JOINED.
EWEL, M22774, AAA30500.1, JOINED.
                 556
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. M19372; AAA30500.1; -
. M1422; AAA30500.1; JOINED.
. M19366; AAA30500.1; JOINED.
. M19367; AAA30500.1; JOINED.
. M19368; AAA30500.1; JOINED.
                                                                                  PRT;
535 IGAGVPAAKSAAKAAAKAQFR
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71.5%;
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                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                             Bovinae, Bos.
NCBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                  splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Coll. Relat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 FGGQQPGLPLGYPIKAPKLPAGYGLPYKTGKLPYGFGPGGVAGSAGKAGYPTGTGVGPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               68.8%; Score 1842.5; DB 1; Length 747; 68.9%; Pred. No. 2.7e-66; ive 27; Mismatches 69; Indels 79;
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                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform 3).
/FTId=VSP 004240.
MRS. -> MAG (in Ref. 2 and 3).
E -> G (in Ref. 2 and 3).
633C03E411643D83 CRC64;
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                                               VGGVPGVGISPEAQAAAAKAAKYGVGTPAAAAKAAKAAQFGLVPGVGVAPGVQVAPPG
                                ---VGVPGAGVPGVPGAGIP--VVPGAGIPGAAVPGVVSPEAAAKAAAKYGARPG
                                                                          363 VGVGGIPTYGVGAGGFPGFG------VGVGGIPGVAG-VP---SVGGVPG
                                                                                                                                                            VGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae;
                                                                                                                                                                                  460 VGVVPGVGVAPGIGLGPG------GVIGAGVPAAAKSAAKAAAKAQFR
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85280426; PubMed=2992576; Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S., Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.; Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.5%; Score 1808.5; DB 2; Length 707; 71.5%; Pred. No. 6e-65; Live 21; Mismatches 54; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60346 MW; FDFD559BAB34CE33 CRC64;
                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin; NCBI gi: 163002 (Fragment).
                                                                                                                                                                                                                                          707 AA
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SEQUENCE 707
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AAA30498.1; JOINED.
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M22775; AAA30498.1; JOINED.
M22988; AAA30498.1; JOINED.
M23010; AAA30498.1; JOINED.
                                                                                                                                          419 VGGVPGVGI-----
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Best Local Similarity 71.5
Matches 381; Conservative
                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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M19369;
M19370;
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M22771;
M22772;
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                                                                                                            60 LGVGGIGGVGGLGVSTGAVVPQLGAGVGAGVKPGKVPGVGLPGVYPGGVLPGAGARFPGI
                                                                                                                                                  GVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTT
                        120 GVLPGVPTGAGVKPKAPGGGGAFAGIPGVGPFGGQQPGVPLGYPIKAPKLPAGYGLPYKT
                                                                                                                                                                                                                            198 GKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAKFGAGAAGVLP--GVGGAG
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STRANIE-CSPEL/CA1 TISSUE=Thymus;
The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
GALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVADAAAYK-AAKAGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEM full-length enriched
library, clone:A630042119 product:elastin, full insert sequence
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 VGVAPGVGLAPGVGVAPGGVGVAPGGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
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STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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KIANINE-VEN/N, TISSUE-Mammary tumor. C3;

KIANINE-Z238627; PubMed=12477932;

KIANINE-Z238627; PubMed=12477932;

KIANINE-Z238627; PubMed=12477932;

KIANINE-Z238627; PubMed=12477932;

KIANINE-K.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschenko L., Marushina K., Farmer A.R., Rubin G.M., Hong L.,

Diatchenko L., Marushina K., Farmer A.R., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Robards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Glübs R.A.,

Redelton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Mones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                    STRAIN=C55BL/6J; TISSUE=Thywnus; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; proparatization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tagami M.,
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                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/64; TISSUE=Thymus; MEDLINE=20530913; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Natsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikwa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riki integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK041860; BAC31084.1;
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EMBL; AK051864; AAH51649.1;
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GO; MGI:95317; Bln.
GO; GO:0007519; P:myogenesis; IMP.
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STRAIN-FVB/N; TISSUE-Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Thymus;
50,770 full-length cDNAs.";
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                           Nature 420:563-573(2002)
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SEQUENCE FROM N.A.
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AQFGLVPGVGVAPGVGVAPGVGVAP---GVGLAPGVGVAPGVGVAPGVGVAP-GIGPGGV 498
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
GO:0043149; P.stress fiber formation; IMP.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                            143;
                                                                                                                                             DB 2; Length 860;
                                                                                                                                           ; Score 1731.5; DB 2; Length
; Pred. No. 7.9e-62;
15; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                     LGAGLGAFPAVTFP--GALVPGGVADAAAAYK-AAKAGAGLGGVPGV
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MEDLINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
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01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Matches 396; Conserv
                                                                                                           860 AA;
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                                                               FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely. SUBUNIT: The polymeric elastin chains are cross-linked together
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"Use of an intron polymorphism to localize the tropoelastin gene t
mouse chromosome 5 in a region of linkage conservation with human
                                                                                                              into an extensible 3D network.
--- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
--- PIM: The crosslinks are made of deaminated Lys.
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Elastin.
By similarity.
; 0COBESAAEIEDD7F1 CRC64;
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InterPro; IPR003979; tropoelastin.
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                                                 Genomics 23:125-131(1994).
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nes 395; Conservative
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MEDLINES 88330868; PubMed=2971041;
MEDLINES 88330868; PubMed=2971041;
MEDLINES 883.0868; PubMed=2971041;
MEDLINES 883.0868; PubMed=2971041;
"Rat tropoalastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
-! FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-! SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
-! SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=91104868; PubMed=1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:9677-9683 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=92241859; PubMed=1572637; Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.; Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franzblau C., Pratt C.A., Faris B., Colannino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.; "Role of tropoelastin fragmentation in elastogenesis in rat smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=099372-5; Sequence=VSP_004244; VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=299372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rich C.B., Foster J.A.,
"Characterization of rat heart tropoelastin.";
Arch. Biochem. Biophys. 268:551-558(1989).
                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Blastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                      864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q99372-3; Sequence=VSP_004245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q99372-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 264:15115-15119(1989)
499 AAAKSAAKVAAKAQLR
                                591 PAAAKSAAKAAAKAQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22-31 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Senomics 12:651-658(1992).
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2913947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2768256;
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                                                                                                                ELS RAT 099372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GGIPGV--AGVP----SVGGVPGVGGVPGVGISPEAQAAAAKAAKYG 427
                                                                                                                                                                                                      428 VGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGV 487
                                                                                                                                                                                                                           Y-----GVAGAGGKAGYPTGTGVGSQAAAAAA--KAAKYGAGGAGVLPGVGGGGIPGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GIGGIGGLGVSTGANVPQVGAGIGAGGKPGKVPGVGLPGVYPGGVLPGTGARFPGVGVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AGLGAL--GGGALGPGGKPLKP-----VPGGLAGAGLGAGLGAFPAVTFP--GAL
-AGIPVVPGAGIPGAAV---PGVVSPEAAAKAAAKX
                               377 GIPGVGIPGVGGIPGVGGIPGVGGIPGVGGPGIGGPGIVGGPGAVSPAAAKAAAKA
                                                                                                      ---GIPTYGVGAGGFPGYGVGAGAGLGGASQAAAAAAAAAKAAKYGAGGAGTLGG
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GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
Interpro; IPR003979; tropoclastin.
PRINTS; PR01500; TROPOCLASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                    494 IVPGAVPGALPGAVPGALPGAVPGAVPGTGGGVPGAG----TPAAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.1%; Score 1637.5; DB 2; Length 810; 63.7%; Pred. No. 4.2e-58; ive 13; Mismatches 61; Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Green B.D.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                            593 GLVPGDLGGAGTPAAKSAAKAAAKAOYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VPGGVADAAAYK-AAKAGAGLGGVPGV
                                                                          GARPGVGVGGIPTYGVGAGGFPGFGVGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 24,
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381; Conservative
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            314 GVPGVGVPG-
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG-VSP 004244.
Missing (in isoform 3, isoform 5, isoform 6 and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTIG=VSP_004245.
Missing (In isoform 4, isoform 6, isoform 3 and isoform 8).
/FTIG=VSP_004246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 PYTNGKLPY-----GVAGAGGKAGYPTGTGVGSQ-AAVAAKAAKYAGAGGGGVLPGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 AGVPGVPGALPGIGGIAGVGTPAAAAAAAAAAKYGAAAGLVPGGPGFGPGVVGVPGA
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                                                 VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
Elastin.
By similarity.
Missing (in isoform 2, isoform 5, 7 and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5%; Score 1675.5; DB 1; Length 864; 60.9%; Pred. No. 1.3e-59; ive 17; Mismatches 78; Indels 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456894BB09E79FD4 CRC64;
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                 IsoId=099372-7; Sequence=VSP_004244, VSP_004246;
                                                   Isold=099372-8; Sequence=VSP_004244, VSP_0045
PTM: The crosslinks are made of deaminated Lys
                                                                                                                                                                                                                                                                           M86372; AAA42271.1;
M86355; AAA42271.1; JOINED.
M86363; AAA42271.1; JOINED.
M86364; AAA42271.1; JOINED.
M86376; AAA42271.1; JOINED.
M86376; AAA42271.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003979; tropoelastin.
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Best Local Similarity 60.9
Matches 383; Conservative
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RGD; 67394; E
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                                          Name=8
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AIPGIGGIAGAGTPAAAAAKAAAKAAKYGAAGGLVPGGPG-----VRLPGAGIPGVGGI 348
                                                                                                       405
                                                                                                                                                      426
                                                                                                                                                                                           -----GLGGA-----SP-AAAAAKAAKYGAGGAGALGG 445
                                                                                                                                                                                                                                                                                  446 LVPGAVPGALPGAVPAVPGAGGVPGAGTPAAAAAAAAAAAAAKAGLGPGVGGVPG-GV-- 502
                                                                                                                                                                                                                                          -----GVGTPAAAAKAAAK-AAQFGLVPGVGVAPGVGVAP 461
                                                                                                                                                                                                                                                                                                                                 GVGVAP---GVGLAPGVGVAPGVGVAPGVGVAP-GIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                                                                                                                                                                                          GVGGIPGGVGVGGVPG-GVGPG-GVT-GIGAGPGGLGGAGSPAAAKSAAKAAYK 557
                                                                                                                                     377 GFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISFBAQAAAAAKAAKY------
                                                 PG-AGIPVVPGAGIPGAAV---PGVVSPEAAAKAAAKYGARPGVGVGGIPTYGVGAG
                                                                                           PGVGGIPGVGGPGIGGPGIVGGPGAVSPAAAKAAAKAAKYGARGGV---GIPTYGVGAG
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88028442; PubMed=3665402;
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 1607.5; DB 2; Length 650; 65.9%; Pred. No. 5.7e-57; Live 19; Mismatches 52; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K., "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last annotation
Elastin-CBEL1; NCBI gi: 163003 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Relat. Res. 7:235-247(1987)
M19372; AAA30499.1; -.
M11422; AAA30499.1; JOINED.
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AAA30499.1; JOINED.
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EMBL; M23010; AAA30499.1; JOINED.
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NON TER 1 1
SEQUENCE 650 AA; 55373 MW;
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Best Local Similarity 65.9%
Matches 351; Conservative
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Indels 111; Gaps

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GALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVADAAAYK-AAKAGA--

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60 LGVGGIGGVGGLGVSTGAVVÞQLGAGVGAGVKÞGKVÞGVGLÞGVYÞGGVLÞGAGARFÞGI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVGGIPTYGVGAGGFPGFG------VGVGGIPGVAG-VP----SVGGVPG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 VPGVGVPGVGVPGVGVPGVPGVPGVPGVPGVPGVPGAVSPAAAKAAAKAAKGG324
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198 GKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAKFGAGAAGVLP--GVGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 VPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAAAAAAAGI----VP--GGPGFG-PGV-
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MEDLINE=88028442; PubMed=3665402;
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
splicing.";
Coll. Relat. Res. 7:235-247(1987).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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MEDLINE-85280426; PubMed=2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Elochemistry 24:3075-3080(1985).
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24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence u
Elastin-CBEL3; NCBI gi: 163005 (Fragment).
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M19368; AAA30501.1; JOINED.
M19370; AAA30501.1; JOINED.
M19370; AAA30501.1; JOINED.
M22771; AAA30501.1; JOINED.
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                                                                                                                                                                                                                85 -GLGGVPGVGGLGVSAGAVVPQ----PGAGVKPGKVPGVGLPGVYPGGVLP--GARFPGV
                                                                                                                                                                       28 GALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVADAAAYK-AAKAGA--
                                                                                                                                                                                           -------GVGPQ-AAAAAAAKLGAGGAGVLPGVGVAGGAG
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                                               Hypothetical protein PSEC0191.
Hypothetical protein PSEC0191.
Homo sapiens (Human).
Eukaryota, Metakoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Whole embryo;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K.,
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (Mar-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075494; BAC11651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    -VGVGGIPGVAG-VP-
                                                                                                                              DB 2; Length
                                                                                                                                                    Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                    55;
                                                                                                                               59.9%; Score 1606.5; DB 65.8%; Pred. No. 6.3e-57;
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                                                                                                                                                    21; Mismatches
 EMBL, M22772; AAA30501.1; JOINED.
EMBL; M22773; AAA30501.1; JOINED.
EMBL; M22774; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                       VGVGGIPTYGVGAGGFPGFG---
                                                                                                                                 Query Match 59.9
Best Local Similarity 65.8
Matches 352, Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                              Gaps
GO:0005578; C:extracellular matrix; IEA.
GO:0005201; F:extracellular matrix structural constituent; IEA
                                                                                                                                                                                                                                                                                               27 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGA-
                                                                                                                                                                                                                                 Indels 226;
                                                                                                                                                                                      Length 472;
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                                                                                                                                          472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
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  GO, GO:0005578; C:extracellular matrix; 124.
GO; GO:0005201; F:extracellular matrix structural (InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003379; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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                                                                                                                                                                                    49.0%; Score 1314; DB 2;
55.1%; Pred. No. 2.2e-45;
iive 3; Mismatches 2;
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01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
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MEDLINE=87242320; PubMed=3593675;
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Biochemistry 26:1497-1503(1987)
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                                                                                                                                                                           Arch. Biochem. Biophys. 256:455-461(1987).

-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                     Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T., "Sequence analysis of elastin cDNA from chick aorta and tissuespecific transcription of the elastin gene in developing chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
Structural protein.
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SIGNAL <1 24
                                                                                                                                                                                                                                                                                                                                Isold=P07916-1; Sequence=Displayed;
Name=2; Synonyms=Embryonic;
Isold=P07916-2; Sequence=VSP 004241, VSP 004242;
PTM: The crosslinks are made of deaminated Lys.
               Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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By similar Allysine (Allysine (A
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   MEDLINE=88309083; PubMed=2841924;
                                                             [3]
SEQUENCE OF 457-750 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GLAPGVGGLAPAVGGLAPGVGGLVPGVGGLVPGVGGLAPGV
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/FILL-VST_OVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGVPGAIP-GGVPGGVFYPGAGLGALG---GGALGPGGKPLKPVPGGLAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86; Indels
                                                                                                                                                                                                                                              (Potential)
(Potential)
(Potential)
(Potential)
                                                                                                                                           (Potential)
(Potential)
(Potential)
                                           Potential)
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                                                                                                                 Potential)
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          [Potential]
                                                                                                                                                                                                                                                                                                                                                                                                Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform 2).
/FTId=VSP 004241.
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Allysine
G -> GLGG
Allysine
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571
610
654
667
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571
610
654
667
667
750 AA;
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1953 AA; 159383 MW; C82B4DACD043C3BD CRC64;
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                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001
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                                         Local Sim
Les 233;
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    SEQUENCE
                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLP--GARFPGVGVLP 141
                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                                                                                                                                                                                                                                                      GGKPLKPVPGGLAGAGLGAGTGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLGGVP--
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                 MEDLINE=21621082; PubMed=11751201; Sekhon H.S., Keller J.A., Proskocil B.J., Martin E.L., Spindel E.R., Sekhon H.S., Keller J.A., Proskocil B.J., Maternal nicotine exposure upregulates collagen gene expression in "Maternal nicotine exposure upregulates collagen gene expression in fetal monkey lung. Association with alpha7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21179804; PubMed-11283372; Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.; Extreme diversity, conservation, and convergence of spider silk fibroin sequences."
                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcesy J.B., Hayashi C.Y.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF350276; AAK30605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                     172 AA; 15224 MW; 4980EF4C5AF3330B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TIEMBLrel. 24, Last annotation update)
Major ampullate spidroin 2-like protein (Fragment).
                                                                                                     (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.3e-25;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                     Am. J. Respir. Cell Mol. Biol. 26:31-41(2002)
EMBL; AF230927; AAK14974.1; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1953 AA
                                                                     172 AA
                                                                                                                                                                                                                                                                                                                                                             Score 797.5;
          566 GGLAPGVGAVPGV--GGPAAAAKAAAKAA
                                                                                            Created)
                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nephila inaurata madagascariensis
                                                                                                                                       Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                              29.8%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 291:2603-2605(2001)
                                                                                            (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                      PRELIMINARY;
                                                                                                                                                                             Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                             172
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                               astin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1953
                                                                                                                                                                                        NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                        Matches 155;
                                                                                              01-JUN-2001
                                                                                                                   01-OCT-2002
                                                                                                                                                                                                                                                                                   receptors."
                                                                                                         01-JUN-2001
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                                                 RESULT 28
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1273 GQQGPGGPGAAAAAAAAAGRGPG-GYGPGQGPGGPGAAAAAAGPG-GYGPG-QQGPGAAA 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1154 AAGPGGYĞPGQQĞTGAAAAAAĞĞĞAĞĞYGPGQQGPGGPGAAAAAAGPGĞYĞPĞQQĞ-PĞ 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1213 AAAAAAAGSGPGGYGPGQQGPGGSSAAAAAAGPGRYGPGQQGPGAAAAAAAGSGPGGYGP 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1036 PGQQGPGQGPGGSGAAAAAAGRGPGGYGPGQQGPGGPGAAAAAAGPGGYGPGQQG-PGA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AAAKAAQFGLVPGVGVAPG------VGVAPGVGVAPGVGLAFGVGV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PGFGVGVGGIPG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GVPGVGVPGAGIPVVPGAGIPGAAVPGVVSP-----EAAAKA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 GPGGYGPGQQPGGSGAAAAAAGRGPGGYGPGQQGPGGPGAAAAAAAGRGPGGYGPGQQG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 PGQQGPGGSGAAAAAAGRGPGGYGPGQQGPGAAAAAAGPGGYGPGQQGPGAAAAAA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PGFGPGVVGVPGA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AKEGAGAAGULPGVGGAGVPGVPGVPGILPGIG-----GIAGVGTPAAAAAAAAAAAAKYG 291
                                                                                                                                                                                                                                                                                                   742 AGRGPGGYGQGQGPGGPGAAAAAAGPGGYGPGQGGPGAAA--AAAAGSGPGGYGPGQQG 799
                                                                                                                                                                                 2 GVPGAI-----PGGVPGGVFYPGA-----GLGALGGGALGPGGKPLKPVPGGLAGAG 48
                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 -PIGAGVKPKAPGVGGAFAGIPGVGPFG-GP---OPGVP-LGYPIKAPKLPGGYG----
                                                                                                                                                                                                                                                                                                                                                                                                                            800 pgrsgaaaaaaaaaaggg-gygpgogpggpgaaaaaagggggggggggggaaaaasagr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LPYTTGKLPYGYGPG----GVAGAAGKAGYPTGTGVGPQAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GSGPGGYGPGQPGGPGAAAAAGRGPGGYGPGQQGPGGPGAAAAAGRGPGGYG
                                                                                                                                                                                                                                                                                                                                                                   90 PGVGGLGVSAGAVVPQPGAGVKPCKV----PGVGLPGVYPGGVLPGARFPGVGVLPGV--
                                                                                                                                                                                                                                                 --AGLGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLGGV-----
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Argiope Trifasciata (Banded garden spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Argiope.
                                                               204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAGVPSVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGVGT--PAAAAAK---
   Length 1953;
22.9%; Score 614; DB 2; Length 19
33.8%; Pred. No. 4.1e-17;
ive 16; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1330 AAAAGSGPG-GYGPGQQGPGGPGAAAAAA 1358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAKAAKYG-ARPGVGVGGIPTYGVGAGGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 APGVGVAPGVGVAPG-IGPGGVAAAAKSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last and Flagelliform silk protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, Created)
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                                                                            Conservative
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Gaps 39;
                                                                                                                                                                                                                                                                                                          98 SAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGV--PTGAGVKPKAPG 155
                                                                                                                                                                                                                                                                                                                                                                          SGVTWVESVSVGGAGG--PGAG--GVGPGGVGPGGVGPG----GIYGPGGAG-GLYGPG 162
                                                                                                                                                                                                                                                                                                                                                                                                           156 VGGAF----AGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGYGPG-GV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                          163 AĞGAFGPGGAĞAPĞ-ĞPGGPGFÇĞPGĞ-----LGĞGVĞGAGTGĞ----ĞVĞPĞAĞG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPGVGGAGVPGV-PGALPGIGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 IAGVGTPAAAAAAAAAKAAKYGAAAGLV-PGGPG-----FGPGVVGVPG----- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 FGGAGGPGGPGGPGGAGGGA--GGAGGLYGPGGAGGLYGPGGLYGPGGAGGAGGPGAGGR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 -----AGVPGV-----GVPGAGIPV----VPGAGIPGAAVPGVVSPEAAAKAAAK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 AAKYGARPGV----GVGGIPTYGVGAGGFPGFGVGVGGIPGVAG-------VPSVG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 GV--PGVGGVPGVGISPEAQAAAAKAAKYGVGTPAAAAAKAAAKAAAKAAOFGLVPGVGVAPG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĠAGGPĠAĠĠVĠPGĠVĠP----GGVGPGGIŶĠPĠGAGGLYGPGÀGGÀ--FĠSGGĠAĠ-ÀPĠ 490
                                                                                                                                                                                                                      2 GVPGAIPGGVPGGVFYPGAGLGALG--GGALGPGGKPLKPVPGGLAGAGLGA-----G 52
                                                                                                                                                                                                                                                2 GGPGA--GGAGAGGVGPG-GFGGPGGFGGAGGPGG-----PGGPGGAGGAGGAGGLYG 52
                                                                                                                                                                                                                                                                                53 LGAFPAVTFPGAL-----VPG--GVADAAAYKAAKAGAGLGGY-----PGVGGLGV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.4%; Score 600.5; DB 2; Length 651; Best Local Similarity 38.5%; Pred. No. 7e-17; Matches 225; Conservative 17; Mismatches 201; Indels 141;
                                        SEQUENCE FROM N.A.
Gatesy J.E., Hayashi C.Y.;
Gatesy J.E., Hayashi C.Y.;
Submitted (FRB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF$150264; ARX30593.1;
NON TER
1 152360 MW; 77CEEC8757DE48DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 VGVAPGVGVAPGVGLAPGVGVA-PGVGVAPGVGVAPGIGPGGVA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroin sequences.";
Science 291:2603-2605(2001).
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November 19, 2004, 16:37:11; Search time B.00262 Seconds (without alignments) 2168.321 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Vernet, Corine
Anderson, David
Guo, Xiaojia
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APPLICANT: Miller, Charles
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Gorman, Linda
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Rieger, Daniel
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ORGANISM: Homo sapiens
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Sequence 1, Application US/09964662

Publication No. US20030166846A1

GENERAL INFORMATION:

APPLICANT: FROTBIN SPECIALIES LTD.

APPLICANT: HGC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP

TITLE OF INVENTION: SELF-ALIGNING PROTEINS

TITLE OF INVENTION: OTHER FIBROUS PROTEINS

TITLE OF INVENTION: OTHER FIBROUS PROTEINS

TITLE OF INVENTION: 2003-05-08

CURRENT APPLICATION NUMBER: US/09/964,662

CURRENT FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 1

LENGTH: 731
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Sequence 44, Appl
Sequence 39, Appl
Sequence 40, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR
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TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILNG DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FLING DATE: 2002-03-25
SEQ ID NOS: 4096
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2915
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US-10-720-025-25
US-09-807-742-1
US-09-81-321A-18
US-09-841-321A-18
US-09-888-260-43
US-09-888-260-44
US-09-746-371C-40
US-09-746-371C-40
US-09-888-260-41
US-09-888-260-41
                                                                                                                                        US-09-746-371C-37
US-09-746-371C-38
US-09-888-260-39
US-09-888-260-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2915, Application US/10104047; Publication No. US20030236392A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
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CRGANISM: Homo sapiens
US-10-104-047-2915
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ORGANISM: Homo sapiens
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Best Local Similarity
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        US-10-104-047-2915
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US-09-964-662-1
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APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPBUTIC POLYBEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHORIER REPERBNE: 21402-416 MS/10/210,172
CURRENT APPLICATION WHERE: US/10/210,172
PRIOR APPLICATION NUMBER: 60/309,501
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                                                                                                                     Sequence 2477, Application US/10108260A
; Publication No. 1020040005560A1
; Publication No. 1020040005560A1
; GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT PILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 2477
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'Sequence 40, Application US/10210172

; Publication No. US20040043928A1
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Ji, Weizhen
Jadigaru, Muralidhara
Casman, Stacie
Voss, Edward
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Zerhusen, Bryan
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Malyankar, Uriel
MacDougall, John
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Hjalt, Tord
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 19, 2004, 16:06:25; Search time 2.20393 Seconds (without alignments) 2139.188 Million cell updates/sec on: Run

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1 AAAGLGAGIPGLGVGVPGVPG.....LGVGAGVPGFGAGADEGVRR Title: Perfect score: Scoring table: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

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1: pir1:*
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A;Molecule type: mRNA
A;Residues: 1-860 <MTD>
A;Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
C;Genetics:
A;Map position: 5
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Ny Contains: elastin precursor, splice form b; elastin precursor, splice form c
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 08-Uun-1989 #sequence_revision 26-Uul-1996 #text_change 09-Uul-2004
C; Accession: Al1865; AZ5728; BZ5728; BZ5728; A22343; I45586
C; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams R; Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams A; Reference number: A31865; MUID:89274159; PMID:2543440
A; Reference number: A31865
A; Anolecule type: DNA
A; Residues: 1-27 < VEE->
A; Accession: A31865
A; A; Residues: 1-27 < VEE->
A; Coss-references: UNIPRCT:P04985; UNIPRCT:Q28101; GB:J02855; NID:g340504; PIDN:AAA307
B; Raju, K.; Anwar, R.A.
A; Raju, K.; Anwar, R.A.
B; Raju, K.; Anwar, R.A.
B; Raju, Chem. 262, 5755-5762, 1987
A; Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of A; Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of A; A; Reference number: A92640; MUID:87194772; PMID:3032943
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A, Gross-references: GB: K03505; NID: g163025; PIDN: AAA30505.1; PID: g163026
A, Accession: C26728
A, Molecula type: MRNA
A, Residues: 1, 'RS', 4-11,'E', 13-225,260-636,'V', 638-747 <RA3>
A, Kolecula type: MRNA
A, Residues: 1, 'RS', 4-11,'E', 13-225,260-636,'V', 638-747 <RA3>
A, Kolecula type: MRNA
A, Residues: 1, 'RS', 4-11,'E', 13-225,260-636,'V', 638-747 <RA3>
A, Coss references: GB: K03506; NID: g163027; PIDN: AAA30506.1; PID: g163028
A, Coss references: GB: K03506; NID: g163027; PIDN: AAA30506.1; PID: g163028
A, Title: Structure of the 3' portion of the bovine elastin gene.
A, Reference number: A22343; MUID: 85280426; PMID: 2992576
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A.Cross_references: GB:MZ0415
R.Rosenbloom, J.
Eab. Invest. 51, 605-623, 1984
A.Title: Biology of disease: Blastin: Relation of protein and gene structure to disease A.Reference number: 145885; MUID:85059254; PMID:6150137
                                                                                                                                                                                                                                                                                                                      C.Superfamily: elastin
C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-27/Domah: signal sequence #status predicted <SIG>
F;28-860/Product: elastin #status predicted <MAT>
F;850-855/Disulfide bonds: #status predicted
A, Title: Use of an intron length polymorphism to localize the tropoelastin gene A, Reference number: A55721; MUID:95130069; PMID:7829060
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R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
A;Accession: B26728
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Pred. No. 2.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elastin precursor, splice form a - bovine N,Alternate names: tropoelastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
A, Residues: 678-683, 685-747 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%;
Local Similarity 81.4%;
les 35; Conservative
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A;Residues: 164-453,488-500,507-617,651-792 <FA2>
A;Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
ine oxidase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-453,483-617,651-792 <FAZ>
A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Note: this sequence represents a composite of several splice forms
R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
A;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
A;Title: Isolation and characterization of human elastin cDNAs, and age-associated varia
A;Reference number: A53891; MUID:88156138; PMID:2831431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:U02948
A;Cross-references: Unitalik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
B;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
J. Biol. Chem. 264, 8887-8891, 1989
A;Title: Characterization of the complete human elastin gene. Delineation of unusual fea
A;Reference number: A33705; MUID:89255358; PMID:2722804
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R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant
A;Reference number: A30524; MUID:89009960; PMID:3171221
                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bote: 22-Jun-1990 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A32707; A33705; A36224; A53891
R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, Proc. Natl. Acad. Sci. U.S.A. 84, 580-5684, 1987
A;Title: Alternative splicing of human elastin mndicated by sequence analysis of A;Reference number: A32707; MuID:87289668; PMID:3039501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine F;1-26/Domain: signal sequence #status predicted <SIG> F;27-792/Product: elastin #status predicted <MAT> F;782-787/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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NiAlternate names: tropoelastin
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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R;Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 253; DB 1;
ilarity 100.0%; Pred. No. 7.7e-16;
Conservative 0; Mismatches 0;
                                                              ALIGNMENTS
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A;Map position: 7q11.23-7q11.23
                                                                                                                                                                                                                                            elastin precursor, long splice form - human
N,Alternate names: tropoelastin
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A; Residues: 1-500,507-792 <IND>
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A; Residues: 1-27 <BAS>
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GenCore version 5.1.6
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201927 phytophthor Q6py85 kukulcania Aat08432 kukulcania Q88913 thermoprote Q01914 phytophthor Q6q294 agelenopsis Aat08436 agelenopsis Q813sr9 salmonella Q8194 thermoprote Q9ppk3 xylella fas	V97197 The Table 11 P05790 Dombyx mori 06c312 yarrowia 11 06c337 arabidopsis 091461 mus musculu 074149 anopheles 9 Q80890 herpesvirus Q74186 oryza sativ 09ncn0 plasmodium 08ryp0 penaeus van 06c117 rattus nor Aap4856 rattus norv Aap4856 pasmodium 079591 plasmodium 099468 plasmodium 025715 plasmodium 025715 plasmodium 025715 plasmodium 025788 plasmodium 025788 plasmodium 026948 twulcania Aat0843 kukulcania	Q25946 plasmodium Q25946 plasmodium Q01916 phytophthor Q2260 onobrychis Q7ght5 anophales g Q26616 strongyloce Q1434 nephila cla Q8wrp1 penaeus van Q925h6 mus musculu Q89403 paramecium Q89403 paramecium Q89403 paramecium Q89403 poramecium Q89403 poramecium Q89409 plasmodium Q7x366 homo sapien Q8wrp2 penaeus van Q8wrp2 penaeus van Q8wrp5 penaeus van Q8wrp	Q9bjp4 plasmodium Q9gqx4 plasmodium Q9gqx4 plasmodium Q8awb2 lampetra fl Q44367 mytilus edu Q9sv88 arabidopsis G6dinl xenopus tro Q7v2m3 prochloroco Q820z7 salmonella Q89375 paramecium Q9bjs5 plasmodium Q9ky7 mycobacteri Q4645 lycopersico Q9gub5 galleria me Q9heh4 neurospora O18507 tenebrio mo
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AN DELINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed=12853948; MEDLINE=22737999; PubMed R.S., Fulton R.S., Fulton R.S., Walker R., Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E., Radell G.A., Delehautry K.D., Mince T.L., Nash W.E., Cordes M., Du H., Edwards J., Bradhaw-Cordum H., Ali J., Andrews S., Isak A., Ranbrutt A., Delwes J., Fourtney L., Kalicki J., Ranbrutt A., Holmes A., Harkins R., Harris A., Ratong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S., Ranbrutt A., Mboott A., Minx P., Marray J., Woessner J.P., Thu-wollam A.M., Abbott A., Minx P., Marray J., Woessner J.P., Thu-wollam A.M., Abbott A., Minx P., Marray J., Woessner J.P., Ranbrutt A., Minx B., Marray J., Woessner J.P., Randling T., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L., R. Hitchenbotham M.T., Eldred J., Walliams D., Bedell J.A., Mardis B.R., Allifon S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E., R. Gliftett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K., Rayman E., Levy R., Brent M.R., Reibler E., Flicek P., Bock P., Suyama M., Baartsch R.A., Brent M.R., Roillam B.C., Chirwalla A.T., Gish W.R., R. Marerston R.H., Wilson R.K., Raymosome 7.";

R. With DNA sequence of human chromosome 7.";
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wilson R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC05056; AAS07435.1; -.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001979; tropoelastin.
PRINTS; PRO1507; TROPOELASTIN.
PROSITE; PRO01001; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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100.0%; Pred. No. 1.1e-12;
iive 0; Mismatches 0;
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02-MAR-2004 (TrEMBLrel. 27, Last sed
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Best Local Similarity 100.
Matches 49; Conservative
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Name=ELN;
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GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
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SEQUENCE FROM N.A.
MEDILINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Indik Z., Yoon K., Forstown of the human elastin gene: great abundance "Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";
of Alu repetitive Res. 16:197-211(1987).
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 757 AA; 66136 WW; 23B7FESBBAFB5CA8 CRC64;
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M17266; AAC98395.1; JOINED.
M17267; AAC98395.1; JOINED.
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M17275; AAC98395.1; JOINED.
M17276; AAC98395.1; JOINED.
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M17280; AAC98395.1; JOINED.
M17281; AAC98395.1; JOINED.
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M17278; AAC98395.1; JOINED.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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M17270; AAC98395.1;
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nes 49; Conservative
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M17274; AAC98395.1;
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                                                                             PRELIMINARY;
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Homo sapiens (Human).
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01-NOV-1996
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Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,

While K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

Revell G.A., Delehantry K.D., Miner T.L., Nash W.E., Cordes M., Du H.,

B. Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

Nan H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

A corsex P., Bleilcki L., Scott K., Holmes A., Harkins R., Harris A.,

A Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

A Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

Tin Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,

RA Mendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,

R. Biert T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,

R. Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

Glifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,

S. Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,

Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Purey T.S.,

Samms E., Levy R., Clendenning J., Kaul R., Kent W.J., Purey T.S.,

Balts J.A., Portnowy M.E., Torrents D., Chinwalla A.T., Gish W.R.,

RA Materston R.H., Wilson R.K.,

R. "The DNA sequence of human chromosome 7.",

Nature A. Aller L. All
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
Morris C.A., Keating M.T.;
"Elastin point mutations cause an obstructive vascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 757;
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Du H., Rohlfing T., Strong C.;

"The sequence of Homo sapiens BAC clone CTB-51J22.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.H.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
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0; Mismatches 0;
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01-MAR-2004 (TrEMBLrel. 26, Last anno
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EMBL; U93037; AAB65621.1; -.
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SEQUENCE FROM N.A.
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Best Local Similarity
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               RAPARA RA
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Martindale D.W., Wilson M.D., Mang D., Burke R.D., Chen X.,
Duronio V., Koop B.F.;
"Comparative genomic sequence analysis of the Williams syndrome region (LIMKL-RFC2) of human chromosome 7q11.23.";
Mamm. Genome 11:890-898 (2000).
EMBL; U63721; AAC13884.1; ---
EMBL; U63721; AAC13884.1; ---
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE=96411691; PubMed=8812460;
MEDLINE=96411691; PubMed=8812460;
Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
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                   EMBL; U93035; AAB65621.1; JOINED.

EMBL; U93036; AAB65621.1; JOINED.

GO; GO:0005578; C:extracellular matrix; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR01451; Hexapep_transf.

InterPro; IPR03979; tropoelastin.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                Score 245; DB 2; Length vs.:
Pred. No. 4.3e-12;
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                                                                                                                                                                                                                                                                                                 55279 MW; 72950C364127B2A4 CRC64;
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Last annotation update)
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100.0%; Pred. No. 9.4e-10;
ive 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
EMBL; U93034; AAB65621.1; JOINED.
                                                                                                                                                                                           PR01500; TROPOELASTIN
                                                                                                                                                                                                                                                                                                                                                         96.8%;
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MEDILINE=81274906; PubMed=3038460; Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J., Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J., Ornstein-Goldstein N.; "Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences."; Connect. Tissue Res. 16:197-211(1987).
                                                                                                                                                                                                                                                                                                                                       MOST, FOUNDESTREET CONTRACTOR MATRIX; IEA.

GO, GO:0005578; C:extracellular matrix structural constituent; IEA.

GO, GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR0019451; Hexapep transf.

INTERPRO; IPR001950; TROPOGLESTIN.

PRINTS; PR01500; TROPOGLESTIN.

PROSTITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.

SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69 CRC64;
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Last sequence update)
Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0254.
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Pred. No. 1.9e-09;
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Connect. Tissue Res. 16:12, --

EMBL; M17282; AAC98393.1; --

EMBL; M16983; AAC98393.1; JOINED.

M17265; AAC98393.1; JOINED.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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M17268; AAC98393.1;
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M17273; AAC98393.1;
M17275; AAC98393.1;
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Best Local Similarity
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M17272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
                                                                                                                                                             Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Orsuki T., Sato H., Wakanatsu A., Ishii S., Yamamoto J., Ishoo Y., Kawai-Hio Y., Saito H., Wakanatsu A., Ishii S., Yamamoto J., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugino Y., Nagai K., Isogai T.; Suzuki Y., Sugano S., Nagahari K., Masuko Y., Nagai K., Isogai T.; Suzuki Y., Sugano S., Nagahari K., Submitted (Jul.-2003) Lothe EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
        05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16246.
Hypothetical protein FLJ16246.
Buken sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 212; DB 2; Length 570;
Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mashform Y., Nagai K., Isogai T.;
Mashform CDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK122731; BAC85506.1; -
SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AK122731; BA285506.1, -.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR0013979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN_1.
SEQUENCE 570 AA; 48941 WW; 3117B028D06D4F7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 446
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      Last annotation update)
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Pred. No. 1.7e-09;
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nes 41; Conservative 0; Mismatches
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                                                                                                                    NCBI_TaxID=9606;
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BAC85506;
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RESULT 7 BAC85506

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Length 643;

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PRELIMINARY;

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RESULT 8 Q8NBI4

Best Loca Matches

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Gaps

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Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89009960; PubMed=3171221; Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z., Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.; Cloning of full-length elastin ColNAs from a human skin fibroblast recombinant cDNA library: further elucidation of alternative splicing utilizing exon-specific oligonucleotides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Hippocampus, and Placenta;
MEDLINE-9623139; PubMed-8689688;
Franciscatis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green B.D.,
Procechel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE=87289668; PubMed=3039501;
T-Ait 7 . Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Rosenbloom J.C., Peltonen L., Rosenbloom J., Indicated P., Anderson N., "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nameranno.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'LIM-kinasel hemizygosity implicated in impaired visuospatial
                                                                                                                                                                                                                         Length 711;
                                                                                                                                                                             711 AA; 61765 MW; 95B624A99B4A989B CRC64;
                                                                                                                                                                                                                                                                                                                         547 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 587
                                                                                                                                                                                                                                                                                                  1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                     EMBL, BX537939; CAD97910.1; -ransf.
Interpro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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                                                                                                                                                                                                                  83.8%; Score 212; DB 2;
100.0%; Pred. No. 2e-09;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                     ELS HUMAN STANDARD; PRT; 730 AA. P15502; Q14233; Q14238; 01-APR-1990 (Rel. 14, Created) 1-APR-1990 (Rel. 14, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Elastin precursor (Tropoelastin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Invest. Dermatol. 91:458-464(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM 1).
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Lab. Invest. 58:270-277(1988)
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              TISSUE=Human fetal kidney;
                                                                                                                                                                                                                                     Local Similarity 100.
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INVOLVEMENT IN CUTIS LAXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructive cognition.";
Cell 86:59-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin fibroblast;
                                                                                                                                                          Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
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ELS_HUMAN
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                                                                                                            MSSY; POUDS, 12E.

GO; GO:0005578; C:extracellular matrix; NAS.

GO; GO:003023; F:extracellular matrix constituent conferring. . .; NAS.

InterPro; IPR001451; Hexapep transf.

InterPro; IPR003979; tropoelastin.

PRINTS; PR01500; TROPOELASTIN.

PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.

SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Human rectum tumor;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2e-09;
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                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; EX538199; CAD98065.1; -...
InterPro: IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                       687 AA; 59847 MW; 79232A191DC1F10F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein DKF2p686021208 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                               100.0%; Preq. ...
'''e 0; Mismatches
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EMBL, M17276; AAC98393.1; JOINED.
EMBL, M17277; AAC98393.1; JOINED.
EMBL, M17278; AAC98393.1; JOINED.
EMBL, M17279; AAC98393.1; JOINED.
EMBL, M17281; AAC98393.1; JOINED.
HSSP; P50099; 12FJ.
                                                                                                                                                                                                                                                                                     83.8%;
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                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=DKFZp686021208;
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Best Local Similarity
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SEQUENCE FROM N.A.
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10 072316 072316 072316 07316

Matches

RESULT 11

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RESULT 10

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Genew; HGNC:3327; ELN.

MIM; 130160; -. MIM; 123700; -. MIM; 194050; -. MIM; 185500; -.

HSSP; P50099; 1ZFJ

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                                                                                                                                                                                                                                                                                                                                                            EMBL; M17282; AAC98394.1; -.
EMBL; M16983; AAC98394.1; JOINED.
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EMBL; M17267; P
EMBL; M17268; P
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M17272;
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M17276;
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                                                                                                                                            Name=1;
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EMBL; 1
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EMBL;
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EMBL;
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Namuelar 181502-2; Sequence=VSP 004243; Isolate 195502-2; Sequence=VSP 004243; Isolate 195502-2; Sequence=VSP 004243; Isolate 1958ASE: Defects in ELNA are a cause of autosomal dominant cutis laxa [MIM:123700] Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased characterized by loose, hyperextensible skin with decreased resilience and elasticity leadaing to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis.

--- DISEASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7g11.23 aleletion syndrome stenosis (SvAS) [MIM:185500]. SvAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                        Pubbod=10942104;
Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Boyd C.D.;
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
Figolated supravalvular actric stenosis: functional haploinsufficiency
of the elastin gene as a result of nonsense-mediated decay.";
Hum. Genet. 106:577-58812000).
I-FUNCIION: Major structural protein of tissues such as aorta and
nuchal ligament, which must expand rapidly and recover completely.
SUBUNIT: The polymeric elastin chains are cross-linked together
inc an extensible 3D network.
I-SUBCELIOUAR LOCATION: Extracellular matrix of elastic fibers.
I-ALTERNATIVE PRODUCTS:
MEDLINE-99091639; PubMed-9873040;
Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
"Cutis laxa arising from frameshift mutations in exon 30 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative splicing, Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P15502-1; Sequence=Displayed;
                                                                                                                                                                                 elastin gene (ELN).";
J. Biol. Chem. 274:981-986(1999)
                                                                                                                                                                                                                                                                                                                                        INVOLVEMENT IN SVAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 syndrome.
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Gaps

0

0; Indels

548 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 588

1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA

Length 730;

Score 212; Db 1, No. 2.1e-09;

730 AA; 63260 MW; 83.8%;

725

720

DISULFID VARSPLIC SEQUENCE

7 7 7

SIGNAL CHAIN 100.0%; Pred. ...

41; Conservative

Matches

ð q

Query Match Best Local Similarity

Elastin.
By similarity.
Missing (in isoform 2).
/FTIGH-VSP 004243.
AB06D15BAS67AE46 CRC64;

MIM) 185500; -
GO, GO:0005578; C:extracellular matrix; TAS.

GO, GO:0005578; C:extracellular space; TAS.

GO, GO:0005201; F:extracellular matrix structural constituent; TAS.

GO, GO:0008203; P:cell proliferation; TAS.

GO, GO:00098015; P:organogenesis; TAS.

GO, GO:0009887; P:organogenesis; TAS.

GO, GO:0007585; P:respiratory gaseous exchange; TAS.

InterPro; IPR003979; Iropoelastin.

PRINTS; PR01500; TROPOELASTIN.

Alternative splicing; Connective tissue; Repeat; Signal;

Structural protein; Williams-Beuren syndrome.

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Whole embryo;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S. Saito K., Yamamoto J., Wakamatu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ARC75494; BRC11651.1;
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005578; C:extracellular matrix structural constituent; IEA.
InterPro; IPR001919; Hexapep transf.
InterPro; IPR001979; tropoelastin.
PRNTS; PR01500; TROPOELASTIN.
PRNTS; PR01501, HEXAPEP TRANSFERASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 AAAGLGAGIPGLGVGVGVPCLGVGTGVPGLGVGGGGVPGFGA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGA 41
                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0191.
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82.2%; Score 208; DB 2;
Best Local Similarity 97.6%; Pred. No. 3.1e-09;
Matches 40; Conservative 0; Mismatches 1;
                                                                              472 AA
                                                                                   PRT;
                                                                                       PRELIMINARY;
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RESULT 13
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AAC98394.1; AAC98394.1; AAC98394.1;

AAC98394.1; AAC98394.1; AAC98394.1;

JOINED. COINED JOINED

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AAC98394.1; AAC98394.1;

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JOINED JOINED

AAC98394.1; AAC98394.1;

AAC98394.1;

AAC98394.1;

CAA33627.1; -.

AAB17544.1;

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RESULT 14

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Gaps

0

41

Length 602; 1; Indels

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhath N.K.,
A Hopkins R.F., Jordan H., Moor T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Roback S.A., McEwan P.J., McKernan K.J., Malke J.A., Gunaretine P.H.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madda A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
RA Jones S.J., Marra M.A.;
Ra "Generation and initial analysis of more than 15,000 full-length human
                  Surravalvular aortic stenosis.";
Hum. MOJ. Genet. 6:1021-1028(1997).
EMBL; U93037; AAB65620.1;
EMBL; U93035; AAB65620.1; JOINED.
GO; GO:0005201; F:extracellular matrix; IEA.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR001451; Acapep transf.
InterPro; IPR001451; Acapep transf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
"Blastin point mutations cause an obstructive vascular disease,
                                                                                                                                                                                                                                                                                                                 602
51807 MW; 53B5B9A71EF04807 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFRA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                         PRINTS; PRO1500; TROPOELÀSTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 99:16899-16903(2002)
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97.6%; Pred. No. 7.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 97.6 es 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                     602 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19360; AMASOSOU.; UCLINED.
EMBL; M19367; AAA30SOU.; UCLINED.
EMBL; M19369; AAA30SOU.; UCINED.
EMBL; M19370; AAA30SOU.; UCINED.
EMBL; M19371; AAA30SOU.; UCINED.
EMBL; M22771; AAA30SOU.; UCINED.
EMBL; M22771; AAA30SOU.; UCINED.
EMBL; M22772; AAA30SOU.; UCINED.
EMBL; M22773; AAA30SOU.; UCINED.
EMBL; M22774; AAA30SOU.; UCINED.
EMBL; M22787; EXETRACEILULAR MATRIX; IEA.
GO; GO:0005501; F:extracellular matrix; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88028442; PubMed=3665402; Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.; "Sequence variation of bovine elastin mRNA due to alternative splicing.";
                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UON-2093 (TrEMBLrel. 24, Last sequence update)
01-UON-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBEL2, NCSI gi: 163004 (Fragment).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=85280426; PubMed=2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
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Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.
Morris C.A., Keating M.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAGLGAGIPGLGVGVFGLGVGAGVPGLGVGAGVPGFGAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 AA; 57652 MW; EB3C019E3BD7618D CRC64;
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Last annotation update)
                679 AA
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EMBL, M19372, AAA30500.1; -.
EMBL, M1422; AAA30500.1; JOINED.
EMBL, M19366; AAA30500.1; JOINED.
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
         PRELIMINARY;
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hes 39; Conservative
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01-JAN-1998 (TrEMBLrel.
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                                                                                                                                                                                                         Bovinae; Bos.
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Matches
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RESULT 15

015337

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SEQUENCE FROM N.A.
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                                                                            NCBI_TaxID=9913;
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                                                             Bos.
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SEQUENCE
                                                             Bovinae;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,

Rausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Rales B., Bordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Robkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Mones S.J., Marra M.A.;

R. Meneration and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            Length 658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC06566; AAH65566.1; -. SEQUENCE 658 AA, 56680 WW; SDAFC00D16A2F94E CRC64;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 AAAGLGAGIPGLGVGVGVPGLGVGVPGLGVGVPGFRA 534
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                                                                                                                                                       494 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFRA 534
        SDAFC00D16A2F94E CRC64;
                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                              Score 204; DB 2; L
Pred. No. 8.3e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 204; DB 2;
Pred. No. 8.3e-09;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence 01-NOV-1996 (TrEMBLrel. 24, Last annotation 01-Lastin-CBEL1; NCBI 91: 163003 (Fragment).
                                                                                                                                                                                                                                                                          658 AA
                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                          PRT;
            56680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.6%;
                                                                                                                                                                                                                                                                                                                  02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                80.6%;
llarity 97.6%;
Conservative
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                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
            658 AA;
                                                Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                  ELN protein
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              SEQUENCE
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AAH65566
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Gaps
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88028442; PubMed=3665402;
XPh H., Ornstein-Goldstein N., Todik Z., Sheppard P., Anderson J. Yeh H., Ornstein-Goldstein N., Toosenbloom J.:
Rosenbloom J.C., Ciolla G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
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MEDLINE=85280426; PubMed=2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
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                                                                                                                                                                                                                                  Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.; "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AAAGLPAGVPGLGVGVGVPGLGVGVGVPGLGVGVPGFGA 508
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.7%; Score 199; DB 2; 92.7%; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spliding.";
Coll. Relat. Res. 7:235-247(1987).
Bmbs; M19372; AAA30499.1; JOINED.
EMBL; M11422; AAA30499.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA30499.1; JOINED.
AAA30499.1; JOINED.
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AAA30499.1; JOINED.
                                                                                                                                                                                                            MEDLINE=85280426; PubMed=2992576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M19366; AAA30499.1; JOINED.
M19368; AAA30499.1; JOINED.
M19369; AAA30499.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA30499.1; JOINED.
AAA30499.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M23010; AAA30499.1; JOINED
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Best Local Similarity 92.7
Matches 38; Conservative
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EMBL; M22773; AAA30498.1; JOINED
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P54320;
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SEQUENCE
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Q9ESZ9
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Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J., "Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
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MEDLINE=88028442; PubMed=3665402;
MPLINE=88028442; PubMed=3665402;
No. Anstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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MEDLINE=85280426; PubMed=2992576;

Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;

"Structure of the 3' portion of the bovine elastin gene.";

Elochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 199; DB 2; Length 666;
Pred. No. 2.1e-08;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 AAAGLPAGVPGLGVGVGVPGLGVGVGVPGLGVGVGAGVPGFGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 AA
                                                                    Splicing."; Call Res. 7:235-247(1987).
EMBL; M19372; AAA30501.1; JOINED. EMBL; M19366; AAA30501.1; JOINED. EMBL; M19366; AAA30501.1; JOINED. EMBL; M19369; AAA30501.1; JOINED. EMBL; M19369; AAA30501.1; JOINED. EMBL; M19370; AAA30501.1; JOINED. EMBL; M19370; AAA30501.1; JOINED. EMBL; M23771; AAA30501.1; JOINED. EMBL; M22771; AAA30501.1; JOINED. EMBL; M22773; AAA30501.1; JOINED. EMBL; M22773; AAA30501.1; JOINED. EMBL; M22774; AAA30501.1; JOINED. EMBL; M22775; AAA30501.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elastin; NCBI gi: 163002 (Fragment)
Bos taurus (Bovine).
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2. M19372; AAA30498.1;
2. M19422; AAA30498.1;
2. M19366; AAA30498.1; JOINED.
2. M19367; AAA30498.1; JOINED.
3. M19369; AAA30498.1; JOINED.
3. M19370; AAA30498.1; JOINED.
3. M19370; AAA30498.1; JOINED.
3. M19370; AAA30498.1; JOINED.
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M22771; AAA30498.1; JOINED.
M22772; AAA30498.1; JOINED.
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PRINTS; PR01500; TROPOELASTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 38; Conserv
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NCBI_TaxID=9913;
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EMBL; M22774; AAA30498.1; JOINED.
EMBL; M22775; AAA30498.1; JOINED.
EMBL; M22988; AAA30498.1; JOINED.
EMBL; M23010; AAA30498.1; JOINED.
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005501; F:extracellular matrix structural constituent; IEA.
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELN (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                  Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green E.D.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGA 43
                                                                                                                                                                                               707 AA; 60346 MW; FDFD559BAB34CE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                      810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;
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STRAIN-BALB/c; TISSUE-Lung;
MEDLINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
                                                                                                                                                                                                                                                                                                                            1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       Query Match 78.7%; Score 199; DB 2; Lv
Best Local Similarity 92.7%; Pred. No. 2.2e-08;
Matches 38; Conservative 1; Mismatches 2;
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01-0CT-1996 (Rel. 34, Last sequence update)
05-UUJ-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                   InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
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Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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es 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                             --- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
--- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
--- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
--- PTM: The crosslinks are made of deaminated Lys.
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01-MAR-2003 (TYEWBLrel. 23, Last sequence update)
01-OCT-2004 (TYEWBLrel. 28, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630042119 product:elastin, full insert sequence (Elastin).
 "Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
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                                                                                                                                                                                                                                                                                                                         By similarity.
. OCOBESAAE1EDD7F1 CRC64;
                                                                                                                                                                                                                                                                                        Connective tissue, Repeat; Signal; Structural protein.
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 AA.
                                                                                                                                                                                                                                                                                                     Potential.
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MEDLINE=21085660; PubMed=11217851;
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InterPro; IPR003979; tropoelastin.
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                                                                                                                                                                                                                                                                                                                                      71955 MW;
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hes 35; Conservative
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                                        Genomics 23:125-131(1994).
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The Analysis of the mease transcriptome based on functional annotation of whalysis of the mease transcriptome based on functional annotation of the Marker & 10.1507/1002).

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"The cysteine residues in the carboxy terminal domain of tropoelastin form an intrachain disulfide bond that stabilizes a loop structure and positively charged pocket.";
Biochem. Biophys. Res. Commun. 186:549-555(1992).
--- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
--- SUBUNIT: The polymeric elastin chains are cross-linked together
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing of elastin mRNA in the bovine nuchal ligament."; Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91234332; PubMed=2031719;
Manohar A., Shi W., Anwar R.A.;
"Partial characterization of bovine elastin gene; comparison with the
gene for human elastin.";
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Nuchal ligament;
MEDLINE=89274159; PubMed=2543440;
Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
          GO; GO:0030833; P:regulation of actin filament polymerization; IMP. GO; GO:0041149; P:regulation of actin filament polymerization; IMP. InterPro; IPR003999; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
SEQUENCE 860 AA; 71298 MW; 7C340F2FFFDC92E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Raju K., Anwar R.A.;
"Primary structures of bovine elastin a, b, and c deduced from the
                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
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                                                                                     76.3%; Score 193; DB 2; Length 860; 81.4%; Pred. No. 7.7e-08; ive 1; Mismatches 7; Indels
                                                                                                                                                     608 AAAGLGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGA
                                                                                                                                     1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGTGAGA 43
                                                              71938 MW; 7C340F2FFFDC92E5 CRC64;
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                                                                                                                                                                                                                       ELS BOVIN STANDARD; PRT; 747 AA. P04585; P04986; P04987; Q29421; 13-MG-1987 (Rel. 05, Created) 13-MG-1987 (Rel. 05, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Elastin precursor (Tropoelastin).
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IsoId=P04985-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Biol. 69:185-192(1991),
                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences of cDNA clones.";
J. Biol. Chem. 262:5755-5762(1987).
GO; GO:0007519; P:myogenesis; IMP. GO; GO:0030833; P:regulation of ac GO; GO:0043149; P:stress fiber for
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87194772; PubMed=3032943;
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                                                                                                 Local Similarity 81.4 es 35; Conservative
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Name=2; Synonyms=B; IsoId=P04985-2; Sequence=VSP_004239;

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Alternative splicing; Connective tissue; Repeat; Signal;
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Missing (in isoform 2).
/FTId=VSP_004239.
Missing (in isoform 3).
                        IsoId=P\bar{0}499\bar{5}-3; Sequence=VSP 004240; PTM: The crosslinks are made of deaminated Lys.
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Pred. No. 1.4e-07;
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EMBL; K03505; AAA30505.1; --
EMBL; K03506; AAA30506.1; --
EMBL; J026855; AAA30776.1; --
EMBL; M58652; AAA03519.2; --
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37; Conservative
Name=3; Synonyms=C;
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12
747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A31865; EABO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
400
404
407
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VARSPLIC
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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88330868; PubMed=2971041;
MEDLINE-88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
J. Biol. Chem. 263:13504-13507 (1988)

-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completel-
-!- SUBMUNT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
MEDLINE=91104868; PubMed=1702999;
Medline R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=099372-8; Sequence=VSP 004244, VSP 004245, VSP_004246; PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
splicing.";
                                                                                                                                                                                                                                                                                                     Franzblau C., Pratt C.A., Faris B., Colannino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.;
"Role of tropoelastin fragmentation in elastogenesis in rat smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bvent=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q99372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=099372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
                                                                                                                                                                                                          Rich C.B., Foster J.A.; "Characterization of rat heart tropoelastin."; Arch. Biochem. Biophys. 268:551-558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2;
IsoId=Q99372-2; Sequence=VSP_004244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q99372-3; Sequence=VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=099372-4; Sequence=VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99372-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 264:15115-15119(1989)
                                                                                                                                                                                                                                                                             SEQUENCE OF 22-31 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 12:651-658(1992).
                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A.
                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoforms;
                                                                                                                                                                                                                                                                                                                                                               muscle cells.";
                                                                                                                                                                                                                                                                                            PubMed=2768256;
                                                                                                                                                                                                 PubMed=2913947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
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ij

Gaps

2

7; Indels

Score 181; DB 1; Length 864;

Pred. No. 7e-07;

71.5%; 78.3%;

1; Mismatches

Conservative

Query Match Best Local Similarity Matches 36; Conserv

ò a

completely

456894BB09E79FD4 CRC64;

864 AA; 72786 MW;

SEQUENCE

/FTId=VSP 004245.
Missing (in isoform 4
7 and isoform 8).
/FTId=VSP_004246.

823

809

VARSPLIC

1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEG 46

/FTId=VSP_004244.
Missing (in isoform 3, isoform 5, isoform 6, and isoform 8). Missing (in isoform 2, isoform 5, isoform

308

308

VARSPLIC

By similarity. Missing (in is similarity By simila Elastin.

1 21 864 859 307

<1 22 854 263

DISULFID

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SO PER PETER PETER

SIGNAL

CHAIN

VARSPLIC

PRINTS; PRO1500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal; Structural protein.

IPR003979; tropoelastin.

67394; Eln

InterPro;

A36106;

PIR; RGD;

M86363; AAA42271.1; JOINED. M86363; AAA42271.1; JOINED. M86364; AAA42271.1; JOINED. M86366; AAA42271.1; JOINED. M863671. MAAA7271.1; JOINED.

EMBL; EMBL;

EMBL;

EMBL;

AAA42271.1;

J04035; M86372; M86355;

M86371; AAA42271.1; JOINED. M86376; AAA42272.1; EMBL; M86373; AAA42272.1; JOINED. EMBL; M86375; AAA42272.1; JOINED.

EMBL; EMBL;

EMBL;

4, isoform 6, isoform

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Gaps
                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                  52.0%; Score 131.5; DB 2; Length 1092; 65.9%; Pred. No. 0.0076; cive 4; Mismatches 8; Indels 3;
                                                                                                                 Name=STAG-1;
Theileria taurotragi.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                                               6 GAGIPGLGV-GVGVPGLGV-GAGVPGLGV-GAGVPGFGAGADEG 46
                                                                                                                                                                                                     SEQUENCE FROM N.A.
Skilton R.A., Wassawo D.P.S., Morzaria S.P.;
Submitted (JUN.2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF275878; AAK69409.1;
                                                                                                                                                                                                                                                                                                         1092 AA; 110405 MW; F2AF0B0DE6BF622A CRC64;
                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sporozoite surface antigen STAG-1 (Fragment).
                          PRT; 1092 AA
                                                                                                                                                                                                                                                            InterPro; IPR008845; Sporozoite P67.
Pfam; PF05642; Sporozoite_P67; 1.
NON TER 1092 1092
                                                                                                                                                                                                                                                                                                                                                                        29; Conservative
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                           NCBI_TaxID=27993;
                                                                                                                                                                Theileria.
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Query Match
                                          0964R2;
                             Q964R2
                                                                                                                                                                                                                                                                                                                                                                        Matches
RESULT 26
              Q964R2
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27

RESULT

EMBL; M60647; AAA42269.1; -

3;

Gallus

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-> GLGGFGGQQPGVPLGYPIKAPKLPG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       G -> GVGVPGVGVPG (in isoform 2).
/FIId=VSP 004242.
A -> G (in Ref. 3).
P -> A (in Ref. 3).
P -> A (in Ref. 3).
P -> R (in Ref. 3).
P -> R (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63697 MW; E57ECD60C6EE556F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GAGIPGLGV-GVGVPGLGV-GAGVPGLGV-GAGVPGFGAGA
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 126.5;
  isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                   Allysine
                                                                                                                                                                                                                                                                                                                                                                                                               Allysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sporozoite surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 68.3
28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571
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Best Local S:
Matches 28
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                                                                                                                                                                                                                                                                                                                                                                             Arch. Biochem. Biophys. 256.455-461(1987).
-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polymeric elastin chains are cross-linked together
                                                                                        Garino garino (Girocci).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=87242320; PubMed=3593675;
Bressan G.M., Argos P., Stanley K.K.;
"Repeating structure of chick tropoelastin revealed by complementary
                                                                                                                                                                                                                                                                                                                                                                                                                           into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                           TISSUE=Aorta;
MEDLINE=87297534; PubMed=3502711;
Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
"Sequence analysis of elastin cDNA from chick aorta and tissuespecific transcription of the elastin gene in developing chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01500; TROPOBLASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=Embryonic;
IsoId=P07916-2; Sequence=VSP 004241, VSP 004242;
PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing, Named isoforms=2, Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elastin.
8 X tandem repeats.
1.
2.
                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
        750 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P07916-1; Sequence=Displayed;
                                                                                                                                                                                                                              SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2)
MEDLINE=88309083; PubMed=2841924;
Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A26601; A26601.
InterPro; IPR008160; Collagen.
InterPro; IPR003979; tropoelastin.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                              DNA_cloning.";
Biochemistry 26:1497-1503(1987).
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 457-750 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M18633; AAA48761.1; -.
EMBL; M21880; AAA49082.1; -.
EMBL; M15889; AAA49108.1; -.
       STANDARD;
                                                                                  Gallus gallus (Chicken)
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750
686
127
262
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                                                                                                                               NCBI_TaxID=9031;
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25
83
83
83
     CHICK
                                                                       Name=ELN
               P07916;
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3;

Gaps

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MEDLINE=22120827; PubMed=12125834;
MEDLINE=22120827; PubMed=12125834;
Deppemmenter U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Bhatteacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanosarcina mazei: evidence for lateral gene
                                                     "Mimicry of elastin repetitive motifs by Theileria annulata sporozoite surface antigen.";
                                                                                                                                                                                                                                                                                                       6 GAGIPGLGV-GVGVPGLGV-GAGVPGLGV------GAGVPGFGAGADEGV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                          15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
          MEDLINE=92365719; PubMed=1501630;
Hall R., Hunt P.D., Carrington M., Simmons D.L., Williamson S.,
Tait A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 46.2%; Score 117; DB 2; Length 196; 1 Similarity 57.1%; Pred. No. 0.03; 28; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GLGAGIPGLGVGVPGLGVGAGVPGLGVGAGV-----PGFGAGADEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transfer between Bacteria and Archaea.";

U. Mol. Microbiol. Biotechnol. 4:453-461(2002).

BMBL; AE013279; AAM30238.1;

GO; GO:0005225; F:GTP binding; IEA.

GO; GO:0007049; P:cell cycle; IEA.

InterPro; PR0001451; Hexapep, transf.

PRINTS; PR0423; CELLDVISFTSZ.

PROSITE; PS00101; HEXAPPEP_TRANSFERASES; UNKNOWN_1.

Complete proteome; Hypothetical protein.

SEQUENCE 196 AA; 15462 MW; BB808A7BAC7D028B CRC64;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                           InterPro; IPR000600; ROK.
InterPro; IPR008845; Sporozoite P67.
InterPro; IPR008845; Sporozoite P67.
InterPro; IPR00125; ROK: UNKNOWN 1.
SEQUENCE 907 AA, 91885 MW; 589CE55C740D4835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein MM0542.
OrderedLocusNames=MM0542;
                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                              Query Match 49.6%; Score 125.5; DE Best Local Similarity 50.9%; Pred. No. 0.02; Matches 29; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          196 AA
                                                                                    Mol. Biochem. Parasitol. 53:105-112(1992).
EMBL, M63017; AAA30134.1; -.
PIR; A33934; A33934.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2209;
[1]
        STRAIN-Hissar;
                                                                                                                                                                                                                                                                                                                                                                                                         Q8PZF2;
01-OCT-2002
01-OCT-2002
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Matches
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Q6ZUN2
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559 AA

PRT;

PRELIMINARY;

Q6ZUN2 Q6ZUN2;

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TISSUE=Placenta;
Oshima A., Takenashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakameteu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53787 MW; 20938FFEC5492A01 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein FLJ43523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115; DB 2;
Pred. No. 0.095;
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63.6%; Pred. No. v..
'.. 2; Mismatches
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InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
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Best Local Similarity 63.69
Fig. 28; Conservative
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                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Search completed: November 19, 2004, 16:36:50 Job time : 11.907 secs

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Aay69137 Amino aci
Aay01305 Human tro
Aay01310 Human tro
Aay69068 Amino aci
Aab66657 Human ela
Abu08725 Human ela
Ad196420 Human ela
Ad156653 Synthetic
Aay01301 Amino aci
Aby75223 Human tro
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Amino aci
Human ela
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Human pro
Human pro
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                                                                                                872
1 GVRRSLSPELREGDPSSSQH......LSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Aay601305 F
Aab66656 P
Aab66656 P
Aab66520 F
Aar196420 P
Aay01301 Aaw6615 P
Aaw66115 F
Aaw66115 F
Aaw66115 F
Aaw66113 I
Aay01302 F
Aay01302 F
Aay01302 F
Aay01304 F
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                     2002273 segs, 358729299 residues
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Maximum Match 100%
Listing first 100 summaries
                                                    November 19, 2004, 15:19:20
                                OM protein - protein search, using sw model
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AAX013105
AAX69068
AAX66657
AABG6657
AAX66420
AAX56420
AAX691301
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AAX69130302
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ADM03792
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Human Rat Pi Novel Human Human	135 Amino 071 Amino 307 Human 661 MFU-5	735 Human 424 Human 658 MFU-2.	726 Human 421 Human 316 Non-na	574 Human 575 Human 573 Human	163 New DNA 572 Human s	609 Spider r 610 Spider r	608 Spider r 611 Spider r	571 Human se 413 Human se	704 Glycine- 126 Epstein	137 FLGA Gly 164 Human se	162 Human	343 Epstei	356 Epster 332 EBV te	12 Epstei	81 Human 1 152 Epstein	15 Protei 185 Argiop	97 Spider	46 Nephila	78 Nephil	21 Spider 40 MaSpi s	49 Nephila 84 Argiope	83 ADF-2 s	69 Argiope	11 Human s	44 N. Clav 68 Argiope	53 Spider	50042 N. clav	50047 N. clav	50037 N. clav	30039 N. clav	4308 N.clavi	19738 Protein	19737 Protein	Aam50043 N. clavip Aar99057 Spider dr
ADE40132 ADE56670 ADE08527 AAY01306 AAB88422 AAP82484	AAY AAY AAY AAB	ABU ADL AAB	ABU	ADP	ADP	AAB	AAB	ADP	AAM	ADP3	ADP3	AAYZ	AAB6	AAE3	ADUS	AAE3	AAY4 AAU1	AAWS AAYS	AAW2	ADC3	AAE3	ADC3	AAE3	ADP3	AAE3	AAR9	AAM5	AAM5(AAM5(AAM5	ADP31	AAR14	AAW49 AAW49	AAW49	AAR99
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61 IPGGVVGAGPAAAAAKAAAKAAAÇFGLVGAAGLGGLGGVGGLGVPGVGGLGGIPPAAAK 120

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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated to so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility, to proteolysis is increased. The derivatives have with reduced susceptibility, and can be cased where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative-competitive inhibition of protease activity. The tropoelastin derivative-competition in the protease activity of a medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents of miducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                                                                       Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
Aam50046 N. clavip
Aaw49736 Protein p
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100.0%; Score 872; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 4.5e-58;
Matches 171; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease activity that causes blood clotting
                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 133-134; 136pp; English.
      AAM50046
AAW49736
                                                                                                                                                                                      AAY69137 standard; protein; 171 AA
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          777
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          20.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
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            182.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAO)-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are useful produce the proteins recombinantly. The tropoelastin derivatives nor hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable GAO-binding properties, products. The hybrid protein have controllable GAO-binding properties, peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELDgamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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         rropoelastin; hIE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IPGGVVGAGPAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 872; DB 2; Length 200; 100.0%; Pred. No. 5.2e-58; sive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                           Human tropoelastin derivative SHELgamma.
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                                                                                                                                                                  AAY01305 standard; protein; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Fig 8; 82pp; English.
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Best Local Similarity 100.
Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
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                                                                                                                                      RESULT 2
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The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence consistent of the subsequence of the subsequence has been inserted so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be castagraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease of civity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful for numan or veterinary medicine, cosmetics (e.g. antiwrinkle or hand contropoelastin derivative dorinding chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth cuscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, conditoroytes and platelets. Peptidomimetics that mimic the protease conditions are used for protecting against lung damage caused by the protease, and are used for protecting against lung damage caused by metastases, or to limit protease activity that causes blood clotting
                                                                                                                                                                             Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAKAAKYGAAVPGVLGGLGALGGVG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IPGGVVGAGPAAAAAAAAAAAAAQFGLVGAAGLGGGGGGGGGGGGGGGGGGPPAAAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAGAAVPGVLGGLGALGGVG
                                                                                                                                            Amino acid sequence of a human tropoelastín splice form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 872; DB 3; 100.0%; Pred. No. 1.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 107-109; 136pp; English.
                                          AAY69068 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98AU-00004723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-182399/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ61146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 731 AA;
                                                                                                                                                                                                                                                                                                                                                                                   WO200004043-A1
                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                  Cleavage-site
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                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999;
                                                                                                              30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell growth
                                                                             AAY69068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weiss AS;
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                             AAY69068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins contening the derivatives are useful in medical, wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated tropoelastin derivative SHED26-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPGGVVGAGPAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK 120
                                                                                                                                                                                                                                                   Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVRRSLSPEIREGDPSSSOHLPSTPSSPRVPGALAAAKAGAAVPGVLGGLGALGGVG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macromolecular binding properties, useful e.g. as surgical implants.
                        AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
121 AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New derivatives of human tropoelastin - with elastin-like or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 872; DB 2; Length 216; 100.0%; Pred. No. 5.6e-58; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                    Human tropoelastin derivative SHEL26-36.
                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 35; Page 11; 82pp; English.
                                                                                                                   AAY01310 standard; protein; 216
                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-AU000564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-00008117
                                                                                                                                                                                    (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                     WO9903886-A1.
                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                    07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171;
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                 150
                                                                                                                                                 AAY01310;
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Human elastin mature protein.
      25-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 IPGGVVGAGPAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVGGLGGLPPAAAAK 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVRRSLSPBLREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IPGGVVGAGPAAAAAAAAAAAAAAAPGFGLVGAAGLGGGGGGGGGGGGGGGTPPAAAAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
         IPGGVVGAGPAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGCLGVPGVGGLGGIPPAAAAK 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 731;
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                                                                                                                                                                     Minimal function unit; MFU; human; elastin prosthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               Stahl
                                                                                                                                                     Human elastin protein without signal peptide.
                                                                                                                                                                                                                                                                                                                Rothstein S,
                                                                                                AAB66657 standard; protein; 731 AA
                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN SPECIALTIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 39pp; English
                                                                                                                                                                                                                                                                   99US-00340736.
                                                                                                                                                                                                                                                29-JUN-2000; 2000WO-US017829.
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                               (HSCR-) HSC RES & DEV LP.
                                                                                                                                                                                                                                                                                                                Keeley F,
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-102886/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 731 AA;
                                                                                                                                                                                                              WO200100666-A2.
                                                                                                                                                                                                                                                                                                                  Rothstein A,
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                   29-JUN-1999;
                                                                                                                                     05-APR-2001
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                                                    681
                621
                                                                                                                   AAB66657
                                                                                 RESULT 5
                                                                                         AAB66657
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The invention describes a polypeptide (I) comprising a minimal functioning unit (MFU) which is present in the sequence of human elastin and comprised of at least three beta-sheet/beta-turn structures, and at least construct one amino acid residue that participates in cross-linking, and not construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel creplacement, heart replacement valves and sheets for other uses such as burns or wounds to promote healing. MFUS can be co-aggregated with other proteins, for e.g. collagen, to provide prosthesis material that cresebles the matural structural materials of the body. MFUS modeled on lamprin and other fibrous proteins e.g. spider silk, can be used to make a variety of materials, for a number of different applications, for e.g. cortains are proteins for use in parachutes and in cosmetics. Coating synthetic prosthesis with MFUS modeled on human elastin significantly inhibits platelet binding and activation. The human-like MFU material is more biocompatible than other elastin-containing materials. In contrast corsolubilised fragments of elastin used before, an MFU is a single paractical purposes. Like other elastin preparations, the MFU is non-functionant for experimental and practical purposes. Like other elastin preparations, the MFU is non-immunogenic, thus providing a truly biocompatible material. MFUS modeled con lamprin and other fibrous proteins can be used to make a variety of materials having high tensile strength, elasticity and plasticity of materials them man are and proteins. This is the amino acid sequence of mature human companies are proteins of the invention are based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                beta-sheet/beta-turn structure; fibrous protein; prosthesis; blood vessel replacement; heart replacement valve; burn; wound; lamprin; spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor; platelet activation inihibitor; non-thrombogenic; cell infiltration; non-immunogenic; blocompatible; high tensile strength; elasticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAGAAVPGVLGGLGALGGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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minimal functioning unit; MFU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keeley F, Rothstein S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 naturally occurring fibrous protein.
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PROTEIN SPECIALTIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1B; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00340736.
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Best Local Similarity 100.0
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-391056/37
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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07-AUG-1997;
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                                                                                                                                                                                                                                                      plasticity.
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ABU08725 standard; protein; 731 AA.

RESULT 6 ABU08725 ABU08725;

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IPGGVVGAGPAAAAAAAAAAAAAPGFGLVGAAGLGGLGVGCLGVPGVGGLGGIPPAAAAK 120
                               Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns.
                                                                                                                                                                fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
blood vessel; wound; burn healing; collagen.
                                                   AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                            19. .160
/note= "region specifically claimed in claim 6"
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                                                                                                                                                                                                       Location/Qualifiers
                                                                                                      ADL96420 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Rothstein
                                                                                                                                                  Human elastin protein fragment
                                                                                                                                                                                                                                                                                                            28-SEP-2001; 2001US-00964662.
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                                                                                                                                                                                                                                                                                                                                  97US-00911364
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Keeley F,
                                                                                                                                                                                                                                                                                                                                                       (ROTH/) ROTHSTEIN A.
                                                                                                                                                                                                                                                                                                                                                                       ROTHSTEIN S.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-898105/82.
                                                                                                                                                                                                                                                                               US2003166846-A1
                                                                                                                                                                                                                                                                                                                                                                KEELEY
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                                                                                                                                    20-MAY-2004
                                                                                                                                                                                        sapiens
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07-AUG-1997;
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        561
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                                                                                                                      ADL96420;
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consisting at least three beta sheets/beta turns, and (d) a polypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, a polypeptide having the primary cructure of a portion of a naturally occurring fibrous protein and a secondary structures comprises from and a secondary structures comprises from 3 to about 7 amino acids and the polypeptide is not a naturally occurring throus protein. The minimal functional unit (MFU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood veshel to construct human elastin-like prostheses such as tubes for blood veshel to construct human be co-aggregated with other proteins, con elaing. Alternatively the MFU can be co-aggregated with other proteins, con example collagen, to provide prosthesis material that resembles the collagen, to provide prosthesis material that resembles the subject to infiltration of cells growing in the patient, including conductual materials of the body. The MFU based material is calbacement. The material is more biocompatible than other elastin containing materials proposed for prostheses.
                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                               561 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAKAAKYGAAVPGVLGGLGALGGVG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IPGGVVGAGPAAAAAAAAAAAAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGLPPAAAAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                 1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKYGAAVPGVLGGLGALGCVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic polynucleotide(s) - encode recombinant tropoelastins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 731;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                   100.0%; Score 872; DB 7;
100.0%; Pred. No. 1.8e-57;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tropoelastin; pharmaceutical; surgical dressing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic human tropoelastin (SHEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR56653 standard; protein; 733 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92AU-00006520.
93AU-00009661.
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                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Les 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNSY ) UNIV SYDNEY.
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                                                                                                                                                                                                                                                                                       Sequence 731 AA;
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22-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiss AS,
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR56653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rariants.
                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, metal or synthetic material, where the surface is coated with the polypeptide, a cosmetic material comprising the polypeptide, an elastic comprising the polypeptide, a high tensile strength material comprising the polypeptide a material comprising two or more polypeptide a material comprising two or more polypeptide comprising at least three beta sheet/beta turn structures, (b) a polypeptide consisting essentially of a structures, (b) a polypeptide consisting essentially of a portion of the amino acid sequence of an animal elastin comprising at least three beta sheets/beta turns, (c) a polypeptide consisting essentially of a portion

Claim 5; Fig 1B; 17pp; English.

Length 733;

Sequence 733 AA;

Query Match

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the invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycam (G4G))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are useful to produce the proteins recombinantly. The tropoelastin derivatives have to produce the proteins recombinantly. The tropoelastin derivatives have not hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as urgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL
                                                                                                                                                     ö
                                                                                                                                                                                                                     622
                                                                                                                                                                                                                                                   IPGGVVGAGPAAAAAAAAAAAAAAAGFGLVGAAGLGVGGLGVPGVGGLGGIPPAAAAK 120
                                                                                                                                                                                                                                                                        09
Human synthetic tropoelastin is susceptible to hydrolytic breakdown of the crosslinks. Such material may be useful in e.g. surgical applications, where the gradual loss of material over time is intended. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                    1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                           Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                     121 AAKYGAAGLGGVLGGAGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                        Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of synthetic human tropoelastin SHEL.
                                                                                                                                                       Indels
                                                                                                                                                          0;
                                                                                                                      Score 872; DB 2;
Pred. No. 1.8e-57;
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY01301 standard; protein; 733 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1; 82pp; English
                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-AU000564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97AU-00008117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                         Local Similarity 100.
Les 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-132162/11.
N-PSDB; AAX27704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNSY ) UNIV SYDNEY.
                                                                                             Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9903886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                              Query Match
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Matches
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The present invention relates to the use of an agent that promotes clastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin polymentsation, increasing F:G actin ratio in a smooth muscle cells treating or preventing obstructive vascular disease (e.g. restenosis), or treating or preventing obstructive vascular disease (e.g. restenosis), or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells is useful for decreasing vascular obstruction, promoting vessel by smooth muscle cells, decreasing vascular obstruction, promoting catin ratio in a smooth muscle cell, treating or preventing obstructive actin ratio in a smooth muscle cell, treating or preventing obstructive stenosis. It is also useful in manufacturing a medicament for the treatment or prevention of cclusion of a vessel. The present sequence is treatment propoelastin protein as shown in the exemplification of the
                                   0
                                                                                                                                        61 IPGGVVGAGPAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK 120
                                                                                             Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
                                                                    1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                   Gaps
                                                                                                                                                                                                              AAKYGAAGLGGYLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tropoclastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasctropic.
                                     Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 24; Page 138-141; Opp; English.
                                                                                                                                                                                                                                                                                                                                               ABG75223 standard; protein; 757 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2003; 2003WO-US009391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2002; 2002US-0368084P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tropoelastin protein
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-833516/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing stenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003082203-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
                                                                                                                                                                                                                                                                                                                                                                                      ABG75223;
                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                             683
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                                                                                                                                                                                                                                                                                                                 RESULT 10
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activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease are arthritides, such as rheumatoid arthritis, lupus, amkylosing spondylitis, fibrositis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from

induced arthritis, and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following

induced arthritis;

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Gaps

0

Length 757; Indels

; Score 872; DB 7; ; Pred. No. 1.8e-57; 0; Mismatches 0;

100.0%;

Best Local Similarity 100. Matches 171; Conservative

Query Match

Sequence 757 AA;

9

1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAKAAKYGAAVPGVLGGLGALGGVG 587 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG

646

61 IPGGVVGAGPAAAAAAAAAAAAAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGLPPAAAAK 120

à g à QQ

AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 757 121 AAKYGAAGIGGVIGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171

707

AAW46315

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                                                                                                                                                                                                                                                                               IPGGVVGAGPAAAAAAAAAAAAAAAGFGLVGAAGLGVGGLGVPGVGGLGGIPPAAAAK 120
                                                                                                                                                                                                                                                                                                                      autoimmune disease; arthritide; gene expression analysis; theumatic; theumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antiout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                     09
                                                                                                                                                                 1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                                         GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                             121 AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
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                                                                 Length 757;
                                                                                                                    Indels
                                                                                                                       ;
0
                                                     Score 872; DB 7;
Pred. No. 1.8e-57;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP65160 standard; protein; 757 AA.
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0
                                                        100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2001; 2001US-0336220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                 Conservative
                                                                                Local Similarity
Sequence 757 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003072827-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
                                                                                                           Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2003
                                                        Query Match
                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP65160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP65160
ADP6
AC ADP6
AC ADP6
AX AUD6
AX AUD0
BE Huma
AX AUD0
KW AUD1
KW IMMU

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New non-natural polypeptide with multiple beta-sheet, beta-turn
structures - particularly based on human elastin, useful for coating
prostheses, as wound dressings, etc., allows ingrowth of cells.
                                                                                  functional unit; elastin; human; fibrous protein;
                                                            Human elastin containing non-natural polypeptide MFU-1 sequence.
                                                                                                                                               374. .499
/note= "MFU-1 polypeptide"
                                                                                                                                                                                                                                                                                                        SJ;
                                                                                             beta-sheet; coating; wound dressing.
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Rothstein
AAW46315 standard; protein; 730 AA
                                                                                                                                                                                                                                                                                  HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                        PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 1B; 39pp; English.
                                                                                                                                                                                                                      97WO-CA000560.
                                                                                                                                                                                                                                        96US-0023552P.
97US-00911364.
                                         (first entry)
                                                                                                                                                                                                                                                                                                       FΨ
                                                                                                                                                                                                                                                                                                     Keeley
                                                                                                                                                                                                                                                                                                                          VPI; 1998-145551/13.
                                                                                   MFU-1; minimal
                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                      Rothstein A,
                                                                                                                                                                           WO9805685-A2
                                                                                                                                                                                                                   07-AUG-1997;
                                         23-JUL-1998
                                                                                                                                                                                                                                        07-AUG-1996;
07-AUG-1997;
                                                                                                                                                                                                12-FEB-1998
                    AAW46315;
                                                                                                                                               Protein
                                                                                                                                                                                                                                                                        (PROT-)
                                                                                                                                                                                                                                                                                  (HOSP-)
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and

Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia e

Disclosure; Page; 56pp; English.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT,

Hirsch R, Thorton SL; WPI; 2003-712740/67. GENBANK; NP 000492. The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of

genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-

The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are useful produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, planamacutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, products. The hybrid protein have controllable GAG-binding properties, peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHEEL26-36 excluding exon 26A product

macromolecular binding properties, useful e.g. as surgical implants.

Claim 39; Page 11; 82pp; English.

New derivatives of human tropoelastin - with elastin-like or

Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant. Human tropoelastin derivative SHEL26-36 (excluding exon 26A product) AAY01311 standard; protein; 183 AA 07-JUN-1999 (first entry) WO9903886-A1. Homo sapiens. 17-JUL-1998; 28-JAN-1999 Synthetic. AAY01311; 681 Query Match RESULT 13 AAY0131 Op du à à X289999988888888888888888888888

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putypeptitue into imas at items. Juring by the protein. Bach beta-sheet structure has cont a naturally occurring fibrous protein. Bach beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide can also be derived from the sequences of animal elastin, lamptin and complete same primary structure as part of a natural fibrous protein. They are used to coat prosthesse made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, metal, particularly for use as blood vessel or heart valve replacements. Wound or burn dressings, or stents. They can be used in cosmettic, elastic or high-tensile strength materials, e.g. ropes or parachute cord. Or high-tensile strength materials, e.g. ropes or parachute cord. Prosthesse based on the MFU allow penetration of endothelial cells, so become permanent, living, tissue replacements. The MFU polypeptides have better blocompatibility than known elastin-based materials. They are well defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thromogenic and non-immunogenic. Properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the high exernsibility of elastin and the high tensile strength of spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IPGGVVGAGPAAAAAAKAAAKAAAQFGLVGAAGLGGUGGGGGGGGGGGGGGPPAAAAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           561 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 855.5; DB 2;
Pred. No. 3.1e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.4
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                 New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                     85 OFGLVGAAGLGGUGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGOFPLGGV 144
                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                 25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAA
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                ;
                                                                                                                                                                                           83.1%; Score 725; DB 2; Length 183; 97.3%; Pred. No. 5.4e-47; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 134-135; 136pp; English
                                                                                                                                                                                                                                                                                                             145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                        157 AARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                               AAY69138 standard; protein; 183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98AU-00004723.
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                  143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-182399/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                          Similarity
                                                                                                                                                                              Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200004043-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                    AAY69138;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                      AAY69138
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98WO-AU000564 97AU-00008117

WPI; 1999-132162/11

Weiss AS;

(UNSY) UNIV SYDNEY

.8-JUL-1997;

20010S-0313403P-20010S-0313702P-20010S-0314031P-20010S-0314465P-20010S-0315463P-20010S-0315453P-20010S-03232746P-20010S-032394P-20010S-0340233P-20020S-0354591P-

29-AUG-2001; 17-SEP-2001; 21-SEP-2001;

14-DEC-2001;

05-FEB-2002; 19-MAR-2002; 19-APR-2002; 19-APR-2002;

21-AUG-2001; 23-AUG-2001;

28-AUG-2001;

20-AUG-2001;

20-AUG-2001;

19-APR-2002; 2002US-0373825P. 19-APR-2002; 2002US-0373989P. 23-APR-2002; 2002US-0374632P.

01-AUG-2002; 2002US-00210172

(CURA-) CURAGEN CORP.

002US-0386971P

2002US-0365478P. 2002US-0373814P.

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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that eusceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be contact with serum or wound exudate. The tropoelastin derivatives provide contact with serum or wound exudate. The tropoelastin derivative provide competitive inhibition of protease activity. The tropoelastin derivative-competitive inhibition of protease activity. The tropoelastin derivative-competitive inhibition of protease activity. The tropoelastin derivative-competition in the protease susceptibility sites, are useful in human or veterinary and for inducting chemotaxis. They are also useful for proliferation or competition, particularly of smooth muscle cells, epithelial or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastasses, or to limit or protease activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFGLVGAAGLGGUGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAQQFPLGGV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 PSSPRVPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFGAVPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 725; DB 3;
Pred. No. 5.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.1%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK; Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ; Voss EZ, Boldog FL, Gorman L, Leite MM, Vernet CAM, Anderson DW; Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA; Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;

WPI; 2003-663472/62.

Smithson G;

N-PSDB; ADE40133

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ADE40134 standard; protein; 692 AA
                          Human NOV16b protein - SEQ ID 40.
                   29-JAN-2004 (first entry)
            ADE40134;
RESULT 15
   ADE40134
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NOVX, cardiant, antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective, nootropic, antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzhaimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; 02-AUG-2002; 2002WO-US024483. tissue typing; human; NOV WO2003064589-A2. Homo sapiens, 07-AUG-2003

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2001US-0310291P. 2001US-0310544P. 2001US-0310951P. 2001US-0311292P. 2001US-0311292P.

08-AUG-2001; 09-AUG-2001; 13-AUG-2001; 16-AUG-2001;

2001US-0309501P.

02-AUG-2001; 03-AUG-2001; 07-AUG-2001;

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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, mentidiabetic, immunosuppressive, anti-HIV, gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosolerosis, hypertension, cancer, obesity, diabetes, ADS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546 PGFGAVPGALAAAKAAKKGAAVPGVLGGLGGVGTPGGVGTPGGVVGAGPAAAAAAKAA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV 144
                              treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 PSSPRVPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             606 QFGLVGAAGLGGLGVGGLGVFGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGGFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
polypeptides and nucleic acids, useful for preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%; Score 725; DB 7; Length 692; 97.3%; Pred. No. 1.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 AARPGFGLSPIFPGGACLGKACGRKRK 692
                                                                                                                                                                       Claim 1; SEQ ID NO 40; 560pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 143; Conserva
                                                                                                                  pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 692 AA;
   NOVX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (64G)-binding properties. Cells containing vectors glycosaminoglycan (64G)-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the synthetic human tropoelastin variant SHELdelta26A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                    Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to a derivative or variant of human tropoelastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 OFGLVGAAGLGGLGGVGGVGGVGGGGGPPAAAAKAAKYGAAGLGGVLGGAGGPFLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 725; DB 2; Length 698; Pred. No. 1.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AARPGFGLSPIFPGGACLGKACGRKRK 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                          Human tropoelastin variant SHELdelta26A.
                                    AAY01302 standard; protein; 698 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 2; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.1%;
Best Local Similarity 97.3%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                           97AU-00008117.
                                                                                                                                                                                                                                                                                                                           98WO-AU000564
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-132162/11.
                                                                                                                                                                                                                                                                                                                                                                                          (DNSX ) UNIA SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 698 AA;
                                                                                                                                                                                                                                                                    WO9903886-A1.
                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                             18-JUL-1997;
                                                                                                  07-JUN-1999
                                                                                                                                                                                                                                                                                                  28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          Weiss AS;
                                                                    AAY01302
           RESULT 16
                           AAY01302
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The present sequence represents a numan requered tropoctabelly delight-delight-delight.

C designated SHEL-delight-delight as degenered by removing exon 26a designated SHEL-delight-delight.

C of SHEL (SHEL not defined). The protein is representative of tropoclastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be increased. The derivatives have with reduced susceptibility, e.g. in contact with serum or wound exudate. The tropoclastin derivatives provide contact with serum or wound exudate. The tropoclastin derivatives provide contact with serum or wound exudate. The tropoclastin derivative of derivatives, and other polypeptides containing tropoclastin derivative derivatives, and other polypeptides containing tropoclastin arised for derivative, and the polypeptides containing tropoclastin or derivative, comedicine, cosmetics (e.g. antiwainke or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or conductives in the protease cleavage site in tropoclastin endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. C derivatives are competitive inhibitors of the protease cleavage site in tropoclastin cells derivatives are competitive inhibitors of the protease of the protease, and are used for controlling localized growth of cancers or metastases, or to limit controlling activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human reduced tropoelastin derivative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 QPGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 PSSPRVPGALAAAKAGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAA
                                                                                                                           Tropoelastin, derivative, SHEL-delta-26a, SHEL, proteolysis, protease, antiwrinkle, hand lotion, bulking agent, chemotaxis, proliferation, growth inhibition, peptidomimetic, lung damage, elastin, cancer, metastasis, blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                     Amino acid sequence of a human reduced tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.3%; Pred. No. 1.9e-46;
Matches 143; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 AARPGFGLSPIFPGGACLGKACGRKRK 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 110-112; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98AU-00004723.
30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-182399/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 698 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ61144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200004043-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weiss AS;
                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
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0;

AAY69069 standard; protein; 698 AA.

RESULT 17 AAY69069

à qq ò q Š AAY69069;

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Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PRK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.
                                                                                                                                                                                                                                                                                                                                     In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin
AAO17360 standard; protein; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 15-16; 21pp; German.
                                                                                                                                                                                                                     21-AUG-2001; 2001EP-00250300.
                                                                                                                                                                                                                                          25-SEP-2000; 2000DE-01048633
                                                                                                                                                                                                                                                                                      B,
                                          (first entry)
                                                                                                                                                                                                                                                                                    Haendler
                                                                                                                                                                                                                                                                               Hess-Stumpp H, Haend
Pegidor P, Scotti S;
                                                                                                                                                                                                                                                                                                                  WPI; 2002-317413/36.
                                                                                                                                                                                                                                                               (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 730 AA;
                                                              Human elastin.
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                              EP1191107-A2.
                                        19-JUL-2002
                    AAO17360;
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The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a parient sample and comparing this with the amount of gene product in a control sample. A reduced level is indicative of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin, insulin-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet brind growth factor receptor alpha, laminin M chain, subtilisin like protein PACS4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human elastin

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703

ARPGFGLSPIFPGGACLGRACGRKRK 730 145 AARPGFGLSPIFPGGACLGKACGRKRK

704

AAY01304 standard; protein; 147 AA.

RESULT 20

AAY01304;

SX B

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643
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                                                                                             84
                                                    85 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKYGAAGLGGVLGGAGQFPLGGV
                                        25 PSSPRVPGALAAAKAGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAA
                         Gaps
                        ; 0
83.1%; Score 725; DB 5; Length 730; 97.3%; Pred. No. 2e-46;
                        4; Indels
                     Mismatches
                                                                                                                            145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                    0;
                     Conservative
        Similarity
        Local Simi
hes 143;
                                                              584
Query Match
          Best Loca
Matches
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AARPGFGLSPIFPGGACLGKACGRKRK 730

704

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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual determinist set tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has sytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                              Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 725; DB 8; Length 73
Pred. No. 2e-46;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 2566; 210pp; English.
ADQ19747 standard; protein; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-2003; 2003WO-US038193.
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97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004048938-A2.
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                    26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -0-JUN-2004
                                                                              ADQ19747;
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Matches 14
                                                                      $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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Winterhager E;

Kraetzschmar J, Kreft B,

human; gene therapy; diagnostic marker; pharmaceutical.

12-APR-2002; 2002EP-00008400. 22-MAR-2002; 2002JP-00137785.

EP1347046-A1 24-SEP-2003

Human protein of the invention SEQ ID NO:2477.

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GAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells contending vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELIGAMMMA excluding the product encoded by exon
                                                                         Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a derivative or variant of human tropoelastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VPGALAAAKAAKYGAAVPGVLGGLGGLGGVGTPGGVVGAGPAAAAAAAAAAAAAAAAAAGFGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAKAAQFGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.9%; Score 723; DB 2; Length 147;
100.0%; Pred. No. 6.2e-47;
cive 0; Mismatches 0; Indels
                                              Human tropoelastin derivative SHELgamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGLSPIFFGGACLGKACGRKRK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 FGLSPIFPGGACLGKACGRKRK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Fig 7; 82pp; English
                                                                                                                                                                                                                                                                                                           97AU-00008117
                                                                                                                                                                                                                                                                            98WO-AU000564
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N-PSDB; AAX27706.
                                                                                                                                                                                                                                                                                                                                               (UNSY ) UNIV SYDNEY
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                                                                                                                                                                                                          WO9903886-A1
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                            17-JUL-1998;
                                                                                                                                                                                                                                                                                                             18-JUL-1997;
                                                                                                                                                                                                                                            28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142;
                                                                                                                                                                         Synthetic.
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qq
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                                                                                                                                                                                                                                              Ishii S;
; Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                         New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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0
                                                                                                                                                                                                                                               Otsuki T, Wakamatsu A, Sato H, Is
Ho Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.2%; Score 717; DB 7; L. 96.6%; Pred. No. 7.2e-46; iive 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 AARPGFGLSPIFPGGACLGKACGWKRK 663
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2477; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01303 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                Otsuka M,
                                                                                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                 Hio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarie,
Matches 142; Conservative
                                                                                                                                                                                                                                                 Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                              WPI; 2003-723558/69.
N-PSDB; ADM01349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1999
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Gaps

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07-MAY-2003

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The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated tropoelastin derivative SHELdeltamodified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, pharmaceutical, diagnostic, gene therapy; tissue regeneration;
cell regeneration, membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSSPRVPGALAAAKXGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                          New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 710.5; DB 2; Length 660; Pred. No. 2.2e-45; 0; Mismatches 4; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein encoded by clone NT2RP70003110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634 AARPGFGLSPIFFGGACLGKACGRKRK 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB64761 standard; protein; 617 AA
                                                                                                                              97AU-00008117.
                                                                                                                                                                                                                                                                                                      Claim 7; Fig 3; 82pp; English
                                                                                                    98WO-AU000564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.5%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 96.6
Matches 142; Conservative
                                                                                                                                                                                                               WPI; 1999-132162/11.
                                                                                                                                                         (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                 N-PSDB; AAX27705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 660 AA;
   sapiens
                                          WO9903886-A1
                                                                                                 17-JUL-1998;
                                                                                                                            18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1308459-A2
                                                                      28-JAN-1999
               Synthetic.
                                                                                                                                                                                       Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide enroded by the polynucleotide, an antibody binding to the polypeptide or peptide or its partial peptide, immunologically assaying the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide or the polynucleotide by contacting the polypeptide or peptide or the polynucleotide by contacting the polynucleotide in an expressible manner and an antisense polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide and encoded for detecting the polynucleotide. The polynucleotide and encoded of proteins are useful as pharmaceutical agents and many disease-related genes may be included in their expression and activity, or as targets of genes may be included in their expression and activity, or as targets or regulation of their expression and activity, or as targets or genes therapy. The genes are involved in tissue and/or call creamscription-related proteins, signal transduction-related proteins, contents, signal transduction-related proteins, content of the activity or expression of the encoded protein to treat diseases. The content of the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed content of the invention. Note: Some of the supplied by the content of the invention of the invention of the invention of the content of the invention of the content of the invention of
                                                                                                                                                                                                                                                                 Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590
                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 QFGLVGAAGLGGLGVGGLGGTPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.2%; Score 612; DB 7; Length 617;
85.0%; Pred. No. 5.3e-38;
Live 0; Mismatches 4; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 QFGLVGAAGLGGLGVGCLGVPGVGGLGGIPPAAAKAAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AARPGFGLSPIFPGGACLGKACGRKRK 617
                                                                                                                                                                                          (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 222pp; English.
                                                                    28-MAR-2002; 2002EP-00007401.
                                                                                                                  05-NOV-2001; 2001JP-00379298
25-JAN-2002; 2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as targets of gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125; Conservative
                                                                                                                                                                                                                                                              Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                  2003-450961/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADB62791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 617 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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AC AABO
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AAB08630 standard; peptide; 712 AA

AAB08630

20-DEC-2000 (first entry)

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elastin are used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprising: inhibiting the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cell in vivo; and regulating the migration of smooth muscle cell in vivo; and regulating the migration of smooth muscle cells in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAAAAKAAKYGAAGLGGVLGGAGQFPLGGV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by diminished capacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                   Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human elastin. Peptides derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                   Amino acid sequence of a human elastin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 612; DB 3;
Pred. No. 6.1e-38;
0; Mismatches 4;
                                                                                                                                                                     SVAS; hypertension; transplant arteriopathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 46; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.2%;
                                                                                                                                                                                                                                                                                                                                                               99US-00258217
                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000WO-US002526
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 85.0
nes 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-533134/48
                                                                                                                                                                                                                                                                                                                                                                                                                                           Li DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 712 AA;
                                                                                                                                                                                                                                                 WO200050068-A2
                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         Keating MT,
                                                                                                                                                                                                                                                                                       31-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ID AAB:
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AC AAB:
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compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins inhibiting the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cell in vivo; and regulating the migration of smooth muscle cells in vivo; and regulating the migration of smooth muscle cells in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized by diminished appacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a fusion protein, comprising human elastin and c-myc, preceded by a His tag. The protein is used in compositions of the invention. The specification describes elastin based
                                                             Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAKAAAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFGLVGAAGLGGUGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elastin based compositions useful for treating atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein comprising human elastin and c-myc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.2%; Score 612; DB 3;
85.0%; Pred. No. 6.2e-38;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AARPGFGLSPIFPGGACLGKACGRKRK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AARPGFGLSPIFPGGACLGKACGRKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE40132 standard; protein; 711 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 48; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                    99US-00258217.
                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000WO-US002526
                                                                                                                                                                                                                                                                                                                                                                                                      (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-533134/48
                                                                                                                                                                                                                                                                                                                                                                                                                                             Li DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 730 AA;
                                                                                                                                                                                                                                                         WO200050068-A2
                                                                                                                                                                                                     Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Keating MT,
                                                                                                                                                                                                                                                                                               31-AUG-2000
                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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ID ADE4
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1;

643

84

Gaps

18;

Length 712; 4; Indels 685

PG-

AAB08631 standard; peptide; 730 AA.

AAB08631,

7

Gaps

18;

642 144 684

3

711

84

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Claim 1; SEQ ID NO 38; 560pp; English.
                                                                                                                                                                                                                                                                          Voss Ez, Buruz, Voss Ez, Zhong M, Gerlacu, Guo X, Zhong M, Gerlacu, Edinger SR, Ellerman K, Ma.
                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                   Kekuda R, Miller CE,
                                                                                                                                                                                                                                                                                                            WPI; 2003-663472/62.
                                                                                                                                                                                                                                                                                                                N-PSDB; ADE40131.
                                                                                                                                                                                                                                                                                                                                           pharmacogenomics.
                                                                                  WO2003064589-A2
                                                                                                                                             16-AUG-2001; 2
17-AUG-2001; 2
17-AUG-2001; 2
20-AUG-2001; 2
                                                                                                                              08-AUG-2001;
                                                                                                                         07-AUG-2001;
                                                                                                                                         13-AUG-2001;
                                                                                                                                                                                 28-AUG-2001;
29-AUG-2001;
                                                                       Homo sapiens.
                                                                                                                                    09-AUG-2001;
                                                                                                                                                                  20-AUG-2001;
21-AUG-2001;
          29-JAN-2004
                                                                                                                                                                             23-AUG-2001;
                                                                                                                                                                                            17-SEP-2001;
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                                                                                                                                                                                                      14-DEC-2001;
05-FEB-2002;
                                                                                                                                                                                                                19-MAR-2002;
19-APR-2002;
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ADE40132;
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and

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gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypoptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                583 PGFGAVPGALAAARAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                            85 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                             25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAA
                                                                                                                                                                                                                                                             Score 609; DB 7; Length 711;
Pred. No. 1e-37;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AARPGFGLSPIFPGGACLGKACGRKRK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Protein Q99372, SEQ ID NO 2524
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                           69.8%;
ilarity 84.4%;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                               Sequence 711 AA;
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                                                                                                                                                                                                                                                                                                 124;
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(FARB
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                                                                                                                           cytostatic; anorectic;
                                                                                                              NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic, antidàtabetic; immunosuppressive; anti-HIV; neuroprotective; noctropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; ALDS; multiple sclerosis; tarft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
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Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
                                                                      Human NOV16a protein - SEQ ID 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 2001US-0309501P.
2001US-0310931P.
5 2001US-03109514P.
2001US-0311292P.
2001US-0311292P.
2001US-0313201P.
2001US-0313201P.
2001US-0313415P.
2001US-0313415P.
2001US-0313415P.
2001US-0313415P.
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2001US-0315853P.
2001US-0322716P.
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2002US-0365478P.
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2002US-0374632P.
2002US-0386971P.
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                              (first entry)
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kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal composition of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating continuous and a pharmaceutical composition comprising the one or more polynpeptides or their antibodies. The polynucleotide or the compound that compliant (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNUS) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed form in its inferior in the compound that compound that compound that compound that the compound that the sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 VPGSLAASKAAKYGAAGGLGGPGGLGGPGGLGGPGGPGGPGGVGGVPGGVAGGAP-AAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- GI PGGVVGAGPAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein (useful for identifying genetic disorders) #682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 482; DB 7; Length 864;
Pred. No. 4.3e-28;
8; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841 GGALGALGYQGGGCFGKSCGRKRK 864
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2002US-0365091P.
2002US-0365384P.
2002US-0372381P.
2002US-0372615P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.4
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 864 AA;
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12-APR-2002;
22-APR-2002;
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                                                                                                                                                                 New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                       Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               649 PGFGAVPGALAAAKAAKYGPLPPRASPEDVAVPQPLHLALMQPCLARPTLSVAPEFLASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          709 EQRWWEVEDSPRDPPTSRAGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 AQFG----LVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKYGAAKYGAAGLGGVLGGAGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAKAAAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                                                          Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 475; DB 7; Length 870; 53.5%; Pred. No. 1.5e-27;
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                                                         Tang YT, Asundi V, Goodrich RW, Ren F, Zhang
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P,
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1593; 1177pp; English.
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24-APR-2002; 2002US-0376045P
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.5'
Matches 114; Conservative
                                                                                                                            WPI; 2003-569235/53
                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 870 AA;
                                                                                                                                            N-PSDB; ADE07616
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Weiss AS;
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The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycen (GAG))-binding properties. Cells contending vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiwrinkle or hand lotions, also as surgical implants, foods and industrial produces. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated tropoelastin derivative SHEL31-36 New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants. New derivatives of human tropoelastin Claim 23; Page 10; 82pp; English (UNSY) UNIV SYDNEY WPI; 1999-132162/11

Sequence 60 AA;

Gaps .; 0 36.5%; Score 318; DB 2; Length 60; 100.0%; Pred. No. 7.4e-17; ive 0; Mismatches 0; Indels 60; Conservative Local Similarity Query Match Matches

112 GIPPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171 ð g

AAB88422 standard; protein; 472 AA AAB88422;

membrane or secretory protein clone PSEC0191. Human

(first entry)

23-MAY-2001

Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.

Homo sapiens

EP1067182-A2

10-JAN-2001

07-JUL-2000; 2000EP-00114090.

08-JUL-1999; 99JP-00194179. 11-JAN-2000; 2000JP-00118775. 02-MAX-2000; 2000JP-00183766.

(HELI-) HELIX RES INST.

Ota T, Isogai T,

Hayashi K;

Kawai Y, Sugiyama T,

Nishikawa T,

WPI; 2001-093989/11. N-PSDB; AAF93849

Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development. Nucleic

Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.

which encode human secretory or membrane proteins represented by AABB8317

- AAB88419. Included in the invention are primers AAF93317 - AAF94295 and
AAF62232 - AAF6235 which are used to isolate the CDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The polymucleotide sequences and the protein expression. The
cused in the prevention, treatment and diagnosis of diseases associated
therapy. The polymucleotide sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
cull diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
cull diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
cull diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
cull diagnostic assays (e.g. polymersesion and function of antibodies
cull diagnostic assays (e.g. polymersesion and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
capainst them and in assays to identify modulactors (agonists and
antibodies may also be used as therapeutic agents to down regulate expression and
cattivity. The antibodies may also be used as diagnostic agents for
activity. The antibodies may also be used as diagnostic agents for
cefting the presence of the polypeptides in samples (e.g. by enzyme
cull immunosorbant assay (ELISA). Examples of diseases which may be
considered include rheumatoid arthritis and diabetes 62 PLKP-VPGGLAGA-----GLGAGLGALGGVGIPGGVVGAGPAAAAAAAAAKYG 110 74 80 - AAF93916 28; Indels 128; 25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAA-Length 472; This invention relates to nucleic acid sequences AAF93744 32.1%; Score 280; DB 4; 34.7%; Pred. No. 3.7e-13; 13; Mismatches 90; Conservative Query Match Best Local Similarity 75 -----Sequence 472 AA; Matches

111 AAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAKAA 170 qq 8 g

171 AKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVPGVGGVPGVG ----GAGGT----GABGAG----GTGGIB----81 AKAAQFGLVGAAGLGGL-à g

231 SPEAQAAAAKAAKYGLVPGVGVAPGVGVAPGVGVAPGVGLAP--GVGVAPGVGVAPGVG 288 ----PAAAAKAAKYG-----AAGLG-----GVLGGAGQFPLGGVAARPGFGLSP---115 à 셤

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Search completed: November 19, 2004, 16:28:45

Job time : 37.9467 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 19, 2004, 16:37:11; Search time 27.9275 Seconds (without alignments) 2168.321 Million cell updates/sec Run on:

US-09-743-818A-73

Title: Perfect

872 1 GVRRSLSPELREGDPSSSQH.....LSPIFPGGACLGKACGRKRK 171 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1570615 seqs, 354127592 residues Searched:

1570615 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

PUDLISHER, APPLICATIONS AA:

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1: (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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1: (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

1: (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1: (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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2: (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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4: (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

5: (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

6: (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

7: (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

8: (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

8: (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

9: (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Segmence 1. Appli			Sequence 2477. Ap	Sequence 2915. Ap	Sequence 38. Appl	Sequence 269890.	Sequence 11. Appl	Sequence 2. Appli	Sequence 52. Appl	Sequence 4. Appli	Semience 22. Annl	Sequence 11, Appl
COLUMNIA	ΩI	US-09-964-662-1	US-10-210-172-40	US-09-961-403-8	US-10-108-260A-2477	US-10-104-047-2915	US-10-210-172-38	US-10-424-599-269890	US-09-964-662-11	US-09-964-662-2	US-10-138-098-52	US-10-294-804-4	US-10-225-838B-22	US-10-732-694-11
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	* Query Match	100.0	83.1	83.1	82.2	70.2	8.69	24.8	24.4	24.4	22.4	22.4	22.4	22.4
	Score	872	725	725	717	612	609	216.5	212.5	212.5	195.5	195.5	195.5	195.5
	Result No.	1	2	٣	4	Ŋ	9	7	80	σ	10	11	12	13

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10-414-760-1 10-414-760-1 10-414-760-1 10-460-832-2 19-861-597-6 19-861-597-8 10-414-760-2 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 110-414-760-1 10-411-965-2 110-806-1029-36	10-441 10-443 10-479 10-800 10-800 10-806 10-117 10-117 10-117	10-419-638-5 10-437-638-5 10-80-129-2 10-806-129-19 10-282-122A-10-282-122A-10-282-122A-10-282-122A-10-880-179-3 10-282-122A-10-282-122A-10-282-122A-10-88-122A-10-88-182A-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-10-88-182A-182A-182A-182A-182A-182A-182A-1	84-84 1100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184 100-1184	10 141 - 759 - 16 10 141 - 759 - 16 10 141 - 759 - 16 10 142 - 426 - 16 10 142 - 426 - 16 10 142 - 438 - 12 10 - 479 - 638 - 12 10 - 282 - 122A - 6 10 - 282 - 122A - 6 10 - 123 - 155 - 42 10 - 146 - 731 - 42 10 - 142 - 885 - 128 10 - 142 - 885 - 428 10 - 142 - 885 - 428 10 - 142 - 885 - 428 10 - 158 - 790 - 422 10 - 158 - 790 - 422 10 - 158 - 790 - 423 10 - 158 - 790 - 423
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APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOI FILE REFERENCE: 21402-416 A.
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 OFGLVGAAGLGGLGVGGLGVPGVGGLGGTPPAAAKAAKYGAAGLGGVLGGAGOFPLGGV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 OFGLVGAAGLGGLGVGGLGVFGVGGLGGIPPAAAAKAAKKGAAGLGGVLGGAGGFPLGGG
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SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.1%; Score 725; DB 15; Length 692; 97.3%; Pred. No. 1.3e-44; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-03
PRIOR PELING DATE: 2001-09-21
PRIOR PELING DATE: 2001-09-21
PRIOR PELING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR PLILING DATE: 2001-08-03
PRIOR PLILING DATE: 2001-08-13
PRIOR PLILING DATE: 2001-08-17
PRIOR PLILING DATE: 2001-08-17
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US-09-961-403-8
; Sequence 8, Application US/09961403
                                                                                                                                                                                                                                                             Malyankar, Uriel
MacDougall, John
Stone, David
Alsobrook II, John
                                                                                                                                                      Gerlach, Valerie
Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
                                                                                                                                                                                                                                 Edinger, Shlomit
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Best Local Similarity 97.3
Matches 143; Conservative
                             Boldog, Ferenc
Gorman, Linda
Leite, Mario
Vernet, Corine
                                                                                                      Anderson, David
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                                                                                                                       Guo, Xiaojia
             Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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64763,
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Sequence 64763,
Sequence 325, 2
Sequence 325, 2
Sequence 325, 2
Sequence 325, 2
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Publication No. US20030166846A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BROTEIN SPECIALITES LTD.

APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP

TITLE OF INVENTION: OTHER FIBROUS PROTEINS

FILE REFERENCE: 041082/012

CURRENT APPLICATION NUMBER: US/09/964,662

CURRENT APPLICATION NUMBER: 0203-05-08

PRIOR PILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVG
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                    Sequence
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US-10-141-756-423

US-10-141-759-423

US-10-140-864-423

US-10-142-426-423

US-10-142-426-423

US-10-282-122A-64763

US-10-123-155-35

US-10-146-731-325

US-10-146-731-325

US-10-141-761-325

US-10-141-761-325

US-10-142-885-325

US-10-158-790-325

US-10-158-790-325

US-10-137-811-325

US-10-137-811-325
                                                                                                                                                                                                                                                                                         ALIGNMENTS
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Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Zerhusen, Bryan
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Ji, Weizhen
Padigaru, Muralidhara
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SOFTWARE: Patentin Ver. 2.1
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CRGANISM: Homo sapiens
US-09-964-662-1
 US-10-210-172-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 731
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US-09-964-662-1
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666 AARPGFGLSPIFPGGACLGKACGRKRK 692

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Gaps

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein November 19, 2004, 16:06:25; Search time 7.69127 Seconds (without alignments) 2139.188 Million cell updates/sec Run on:

US-09-743-818A-73

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tropoelatin - she elastin precursor major ampullate fi fibroin heavy chai hypothetical glyci fibroin - Chinese sporozoite surface hypothetical glyci spidroin 2, dragli hypothetical glyci elastin precursor, Description SUMMARIES BAHU 859623 BABS BARD A26601 A26661 A36068 B61013 A36068 B70895 T35389 S760917 E70806 T70806 T70806 T70806 T70806 T70806 T70807 A70812 T31328 A45560 A70514 A44112 E70835 Query Match Length DB 802 489.5 486.4 486.5 486.5 194.5 195.5 197.5 178.5 178.5 178.5 178.5 178.5 178.5 178.5 178.5 178.5 178.5 179.5 170. 168 167 167 167 Score Result No.

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ALIGNMENTS

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tropoelastin - sheep
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Saccession: S59623; A24758
C.Sandoberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Bc
Matrix Biol. 14, 635-641, 1994
A,Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
                                                                                                                                                                                                                                                                                                                                                                 R; Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smit Arch. Biochem. Biophys. 241, 684-691, 1985
A; Title: Analysis of the 3' region of the sheep elastin gene.
A; Reference number: A24758; MUID:85305763; PMID:3839997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mightenate names: tropoclastin

C;Species Mus musculus (house mouse)

C;Decies Mus musculus (house mouse)

C;Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C;Accession: A55721

By Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.

Genomics 23, 125-131, 1994

A;Title: Use of an intron length polymorphism to localize the tropoclastin gene to mouse

A;Reference number: A55721

A;Accession: A55721

A;Accession: A55721

A;Residues: 1-860 *WYD.
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C;Genetics:
A,A,Apa position:
C;Genetics:
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
C;Keywords: alternative splicing predicted <SIG>
F;28-860/Product: elastin #status predicted <NAT>
F;88-0-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 655-669,671-716,732-770 <YOO>
C,Superfamily: elastin
C,Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F,760-765/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 -VGAAGLGGLG-VGGLG-VPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAKAAQFGL- 88
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                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-770 <MAU>
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Pred, No. 4.1e-25;
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                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P11547
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64.5%;
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                                                                                                                                                                                                    A;Reference number: S59623
A;Accession: S59623
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Best Local Similarity
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les 112; Conserv
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A; Residues: 1-453,483-617,651-792 <FAZ>
A; Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A; Note: this sequence represents a composite of several splice forms
R; Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
A; Title: Isolation and characterization of human elastin cDNAs, and age-associated varia
A; Reference number: A53891; MUID:88156138; PMID:2831431
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A;Residues: 164-453,483-500,507-617,651-792 <FA2>
A;Cross-references: GB:M24782; NID:9182063; PIDN:AAAS3190.1; PID:9182064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
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                                                                                                                                                             C; Species: Homo sapiens (man).
C; Species: Homo sapiens (man)
C; Date: 22-Unn-1990 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: A32707; A33705; A30524; A53891
R; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, Proc. Natl. Acad. Sci. U.S.A. 84, 5860-5684, 1987
A; Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of A; Reference number: A32707; MUID: 87289668; PMID: 3039501
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C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-792/Product: elastin #status predicted <MMT>
F;782-787/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 IPGGVVGAGPAAAAAAAAAAAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGPPAAAK 741
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Pred. No. 6.9e-48;
); Mismatches 0;
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A, Map position: 7q11.23-7q11.23
                                                                                                                        elastin precursor, long splice form - human
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100.0%; Pri
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Gezwje homo sapien
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Aah6556 homo sapien
Aah6556 homo sapien
Q72316 homo sapien
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Q28099 bos taurus
Q98031 zattus noru
Q28096 bos taurus
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Q28097 bos taurus
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Q28099 bos taurus
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Q75mu5 homo sapien
Aas07435 homo sapi
Q9umf5 homo sapien
P15502 homo sapien
Q8nbi4 homo sapien
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homo sapien
                                                                November 19, 2004, 15:22:20 ; Search time 34.5734 Seconds (without alignments) 2845.805 Million cell updates/sec
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1 GVRRSLSPELREGDPSSSQH.....LSPIFPGGACLGKACGRKRK 171
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q75MU5
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Q28098
Q9ESZ9
ELS_MOUSE
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR001959; tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87274906; PubMed=3038460; Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J., Rosenbloom J., Ornstein-Goldstein N.; Rosenbloom J., Cregion of the Mission of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences."; Connect. Tissue Res. 16:197-211(1987).
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Indik Z., Yeh H., Ornstein-Goldstein N., Steenbloom J.;
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 757
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SEQUENCE 757 AA; 66136 WW; 23B7FE5B8AF85CA8 CRC64;
                                                                                                                                                        Last annotation update)
                                                                                                                                    Last sequence update)
                                                                      757 AA
                                                                                                                 Created)
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M17268, AAC98395.1; JOINED.
M17270; AAC98395.1; JOINED.
M17272, AAC98395.1; JOINED.
M17272, AAC98395.1; JOINED.
M17273; AAC98395.1; JOINED.
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M17276, AAC98395.1, JOINED.
M17277, AAC98395.1, JOINED.
M17279, AAC98395.1, JOINED.
M17289, AAC98395.1, JOINED.
M17289, AAC98395.1, JOINED.
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EMBL, M17265; AAC98395.1; JOINED.
EMBL, M17266; AAC98395.1; JOINED.
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                                                                      PRELIMINARY;
                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                 (TrEMBLrel.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                     NCBI TaxID=9606;
                                                                                                                 01-NOV-1996
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PERCHENCE FROW N.A.

REDILINE=22737999; PubMed=12853948;

Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Peppin K.H.,

A Wagner-McPherson C., Layman D., Mass J., Jaseper S., Walker R.,

A Wajner K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

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RA Vanbrunt A., Nauyen C., Lamar B., Courtney L., Kalicki J.,

RA Vanbrunt A., Houner S., Toullinson C., Dauphin-Kohlberg S.,

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Rozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

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RA Gillett W., Zhou Y., James R., Pelps K., Iadanotc S., Bubb K.,

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"The DNA sequence of human chromosome 7.";
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 5.9e-41;
ive 0; Mismatches 0; Indels
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, AC005056, AAS07435.1; -.
EMBL, AC005056, AAS07435.1; -.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE, PS001011; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Hypothetical protein.
ENGURNCE. 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
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                                                                                          Last sequence update)
Last annotation update)
757 AA
                                                             Created)
                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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171; Conservative
                                                                                                                                                           Hypothetical protein ELN.
      PRELIMINARY;
                                                                                                                                                                                                                     Homo sapiens (Human)
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                                      Q75MU5;
      Q75MU5
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RESULT 3

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MEDLINE=20458868; PubMed=11003705;
Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
Duronio V., Koop B.F.;
"Comparative genomic sequence analysis of the Williams syndrome region
(LIMX1-RFC2) of human chronosome 7q11.23.";
Mamm. Genome 11:890-898(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJNE=96411691; PubMed=8812460; OSDOINE 17. MAINING DIVINE=96411691; PubMed=8812460; OSDOINE L.R., MAINING D.W., Scherer S.W., Shi X.-M., Huizenga J., Heng H.H.O., Costa I., Pober B., Lew L., Brinkman J., Rommens J., Koop B.F., Tsui L.-C.; "Identification of genes from a 500-kb region at 7q11.23 that is Genomics 36:328-336(1996).
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE-87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                  707 AAKYGAAGLGGVLGGAGQFFLGGVAARPGFGLSPIFPGGACLGKACGRKRK 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 258;
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                                                                                                                                                                                               13, Created)
13, Last sequence update)
26, Last annotation update)
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InterPro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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97.3%; Pred. No. 4e-33;
iive 0; Mismatches 4.
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                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elastin precursor (Tropoelastin).
                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                              Elastin (Fragment).
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Best Local 9
                                                                                                                                            O9UMF5
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                                                                                         RESULT 4
Q9UMF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IPGGVVGAGPAAAAAAAAAAAAAAFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
Du H., Rohlfing T., Strong C.;
"The sequence of Homo sapiens BAC clone CTB-51J22.";
"The sequence of to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005056; AAS07435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
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SEQUENCE 757 AA; 66106 MW; 2B24F955DB360738 CRC64;
                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 5.9e-41;
                                   757 AA.
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                                                                                   Created)
                                   PRT;
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                                                                                                      (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 424:157-164(2003).
                                                                                                                                                          Hypothetical protein ELN.
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.H.;
Submitted (JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2000)
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                 02-MAR-2004
                                                                                                      02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.
                                                        AAS07435;
                           AAS07435
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Tisoid-P15502-2; Sequence=VSP 004243; PTM: The crosslinks are made of deaminated Lys.

PTM: The crosslinks are made of deaminated Lys.

DISPASE: Defects in ELN are a cause of autosomal dominant cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis. DISBASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pubmed=10942104;
Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
Misolated supravalvular acrtic stenosis: functional haploinsufficiency
of the elastin gene as a result of nonsense-mediated decay.";
Hum. Genet. 106:577-588(2000).
-!- FUNCTION: Major structural protein of tissues such as aorta and
nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polymeric elastin chains are cross-linked together
into an extensible 3D network.
-!- SUBCELIULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                        TISSUE-Skin fibroblast,
MEDLINE-89009960; PubMed=3171221;
Fazio M.J., Olsen D.X., Kauh E.A., Baldwin C.T., Indik Z.,
Fazio M.J., Olsen D.X., Kauh E.A.,
Crostein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.,
"Cloning of full-length elastin cDNAs from a human skin fibroblast
recombinant cDNA library: further elucidation of alternative splicing
utilizing exon-specific oligomucleotides.";
J. Invest. Dermatol. 91:458-464(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Hippocampus, and Placenta;
MEDLINE-96291399; PubMed-8689688;
Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99091639; PubMed=9873040;
Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
"Cutis laxa arising from frameshift mutations in exon 30 of the
Rosenbloom J.C., Peltonen L., Rosenbloom J.; "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA."; Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=88156138; PubMed=2831431;
Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
Rosorabloom J., Uitto J.;
"Isolation and characterization of human elastin cDNAs, and age-
associated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keating M.T.; "LIM-kinase1 hemizygosity implicated in impaired visuospatial constructive cognition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P15502-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 274:981-986(1999).
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lab. Invest. 58:270-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 603-730 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elastin gene (ELN).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23. DISBASE: Defects in ELN are the cause of supravalvular aortic stenosis (SVAS). [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:extracellular matrix structural constituent; TAS.
GO; GO:0008283; P:cell prolliferation; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:000887; P:creplation; TAS.
GO; GO:0005887; P:respiratory gaseous exchange; TAS.
GO; GO:0007885; P:respiratory gaseous exchange; TAS.
FINENPRO; IPROOBLASTIN.
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/FIId=VSP_004243.
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Missing (in is
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AAC98394.1; JOINED.
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AAC98394.1; JOINED.
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AAA52382.1;
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Alternative splicing; Connecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 AA; 63260 MW;
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AAB17544.1; -.
CAA33627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M17282; AAC98394.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143; Conservative
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Genew; HGNC:3327; ELN.
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Best Local Similarity
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M36860;
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                                                                                                                                                    syndrome.
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                     EMBL; AK122731; BAC85506.1; ...
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR03379; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN 1.
SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B_CRC64;
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR001975; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TR0POELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN 1.
SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

OLD T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii saito K., Yamamacto J., Wakamatsu A., Nagai T., Nakamura Y., Nagahari K., Sugano S., Isogai T.;

Nagahari K., Sugano S., Isogai T.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AR075554; BAC11696.1; --

HSSP; P50099; 12FU.
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Pred. No. 1.4e-32;
0; Mismatches 5; Indels
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16246.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                      643 AA
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                                                          145 AARPGFGLSPIFPGGACLGKACGRKRK 171
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein PSEC0254. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002
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Q8NB14
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02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakanatsu A., Ishii S., Yamamoto J., Isono Y., Kawai Hio Y., Satto H., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nishikawa T., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Rawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                 442 PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                          25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAKAA
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                                                                         18; Gaps
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Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
               Length 570;
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         Score 612; DB 2; Lv
Pred. No. 1.3e-26;
0; Mismatches 4;
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02-MAR-2004 (TrEMBLrel. 27, Created)
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02-MAR-2004 (TrEMBLrel. 27, Last ann
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            70.2%;
Query Match
Best Local Similarity 85.0°
Matches 125, Conservative
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.P., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Jeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Jeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaybs R.A.,

Willadon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blacksley R.W., Touchman U.W., Grenn E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rizzyminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e-26;
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC065566; AAH65566.1;
InterPro; IPR001451; Hexapep transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSTITE; PR01011; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 658 Aa; 56680 WW; 5DAFC00D16A2F94E CRC64;
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                                                        Last sequence update)
Last annotation update)
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                               05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                    Homo sapiens (Human)
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Matches 125;
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(TrEMBLrel. 27, TrEMBLrel. 27, (TrEMBLrel. 27,

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AAH65566
ID AAH6
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AC AAH6
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AAH65566;

AAH65566

RESULT 10

Homo sapiens (Human)

658 AA

PRELIMINARY;

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(TrEMBLrel. 19, I
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Best Local Similarity 85.03
Matches 125; Conservative
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                                                                      SEQUENCE FROM N.A.
                                       NCBI TaxID=9606;
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01-MAR-2004
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59847 MW; 79232A191DC1F10F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-UUN-2003 (TrEMBLrel. 24, Last anno
Blastin, NCBI 91: 163002 (Fragment).
Bos taurus (Bovine).
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124; Conservative
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                                                                                                Matches 124; Conservative
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         687 AA;
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       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, M17277; AAC98393.1; JOINED.
EMBL; M17279; AAC98393.1; JOINED.
EMBL; M17279; AAC98393.1; JOINED.
EMBL; M17279; AAC98393.1; JOINED.
EMBL; M1728; AAC98393.1; JOINED.
EMBL; M1728; AAC98393.1; JOINED.
GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:003023; F:extracellular matrix constituent conferring. ..; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                       Structure of the 3' region of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";

Connect. Tissue Res. 16:197-211(1987).

EMBL; M17282; AAC98393.1; JOINED.

EMBL; M17265; AAC98393.1; JOINED.

EMBL; M17266; AAC98393.1; JOINED.

EMBL; M17267; AAC98393.1; JOINED.

EMBL; M17271; AAC98393.1; JOINED.

EMBL; M17271; AAC98393.1; JOINED.

EMBL; M17272; AAC98393.1; JOINED.

EMBL; M17272; AAC98393.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Human rectum tumor;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538199; CAD98065.1; ...
Enterpro; IPR001451; Hexapep transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%; Score 612; DB 2; Length 687; 85.0%; Pred. No. 1.5e-26; live 0; Mismatches 4; Indels
                                        MEDLINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO) INTRO 1451; Hexapep transf.
INTERPRO; IPR001451; Hexapep transf.
INTERPRO; IPR0013979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS0010101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OMA-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686021208 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AARPGFGLSPIFFGGACLGKACGRKRK 687
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                                                                                                                                                                                                                                                                                                                                                                 EMBL; M17273; AAC98393.1; JOINED.
EMBL; M17275; AAC98393.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.2
Best Local Similarity 85.0
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
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Q7Z316;
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                                                                                                                                                    559 PGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAATAKAAAKAA
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                                                              18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Wail B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (JUN-2003) to DEML/GenBank/DDBJ databases.

EMBL; BXS37939; CAD97910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
        Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 605; DB 2; Length 711
84.4%; Pred. No. 3.7e-26;
ive 0; Mismatches 5; Indels
69.7%; Score 608; DB 2; Length 68
84.4%; Pred. No. 2.5e-26;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711 AA; 61765 MW; 95B624A99B4A989B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein DKFZp686F06102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          619 QFGLVGAAGLGGLGVGCLGVPGVGGLGGIPPAAAKAAKY-
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1
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ELS MOUSE
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                                                                                                      SEQUENCE
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                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P54320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 QFGLVGAAGLGGLGVGGLG-VPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   654 VAARPGFGLISPIFPGGAGGLGVGGKPPKPFGGALGALGFPGGACLGKSCGRKRK 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS: PR01509; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88028442; PubMed=3665402;
MEDLINE=88028442; PubMed=3665402;
FORBLEIN-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                            Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S., Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.; "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 531.5; DB 2; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         707 AA; 60346 MW; FDFD559BAB34CE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                     "Sequence...
splicing.":
Coll. Relat. Res. 7:235-247(1987).
EMBL; M19372; AAA30498.1;
EMBL; M1936; AAA30498.1; JOINED.
EMBL; M19366; AAA30498.1; JOINED.
EMBL; M19368; AAA30498.1; JOINED.
EMBL; M19369; AAA30498.1; JOINED.
EMBL; M19370; AAA30498.1; JOINED.
EMBL; M19371; AAA30498.1; JOINED.
EMBL; M19371; AAA30498.1; JOINED.
EMBL; M19371; AAA30498.1; JOINED.
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                                                                   MEDLINE=85280426; PubMed=2992576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA30498.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M22774; AAA30498.1; JOINED. M22775; AAA30498.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22773; AAA30498.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M22988; AAA30498.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.5%;
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Best Local Similarity 65.5
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M23010; AAA30498.1;
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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EMBL; AF289665; AAF99336.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AAAKAAKYGAAGLGGVLGGAGOFPLGGVAARPGFGLSPIFP-------- 157
                                                                                                                                                                                                                                                                                                                           -----GGLGVGGLGVPGVGGLGGIPPA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 VPGALAAAKAGAA-----VPGVLGGLGALGGVGIPGGVVGAG-PAAAAAK
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-Lung;
MEDLINE=95130069; bubMed=7829060;
MUDLINE=95130069; bubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
Interbro; IPR003979; tropoelastin.
PRINTS; PR01500; TR0POELASTIN.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                61;
                                                                                                                                                                                          56.1%; Score 489.5; DB 2; Length 810; 55.4%; Pred. No. 1e-19; Live 8; Mismatches 21; Indels 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or senu ...

EMBL, U08210; AAA80155.1; -.

EMBL, U08210; BAMS.

PIR; A55721; EMMS.

ING), MG1:95317; Eln.

InterPro; IFR003979; tropoelastin.

PRINTS; PR01500; TROPOELASTIN.

Connective tissue; Repeat; Signal; Structural protein.
                                                                                                                                             810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                           AAAKAAQFGLVGAAGL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elastin precursor (Tropoelastin)
                                                                                                                                                                                                                           Best Local Similarity 55.4 Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=10090;
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SEQUENCE
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                                                                                                                 116
                                                                                         vPGSLAASKAAKYGAAGGLGGPGGLGGPGGLGGAGVPGRVAGAAPPAAAAAK 719
                                                                                                                           157
                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUB=Thymus; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                ---GGLGVGGLGVPGVGGLGGIPPA
                                                                      30 VPGALAAAKAAKYGAA------VPGVLGGLGALGGVGIPGGVVGAG-PAAAAAK
                                                      Gaps
                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630042119 product:elastin, full insert sequence
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                    61;
                                DB 1; Length 860;
                                                     21; Indels
                                                                                                                                                      117 AAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFP-----
/ similarity.
OCOBESAAELEDD7F1 CRC64;
                               Score 489.5; DB 1
Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                    8; Mismatches
                                                                                                                                                                                                158 -----GGACLGKACGRKRK 171
                                                                                                                                                                                                                    839 ALGALGYQGGCFGKSCGRKRK 860
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PupMed=11217851;
                                                                                                                AAAKAAQFGLVGAAGL-----
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STRAIN=C57BL/6J; IISSUE=Thymus;
The FANTOM CONSOXTium,
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          71955 MW;
                              56.1%;
55.4%;
                                                  Matches 112; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium;
          860 AA;
                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                               Query Match
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STRAINEFURNA.

SEQUENCE FROM N.A.

STRAINEFURNA: TISSUE-Mammary tumor. C3;

MEDLINE=2238257; PubMed=1247932;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfaud G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

T. "Generation and initial analysis of more than 15,000 full-length human

The proper and mouse cDNA sequences "...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanaqaki T., Hara A., Hashizume W., Hayatuno M., Hanaqoki T., Harahizume W., Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki A., Murata M., Ohsato N., Okazuki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Shinata K., Shinata K., Shinata A., Takahashi F., Takawu A., Takahashi F., Takawu A., Takahashi F., Takawu A., Takahashi K., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20530913; PubMed=11076861; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashino H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-171(2000).
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GO; GO:0007519; P:myogenesis; IMP.
GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
GO; GO:0043149; P:stress fiber formation; IMP.
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Pred. No. 1.1e-19;
8; Mismatches 21; Indels 61.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK041860; BAC31084.1; -.
EMBL; BC051649; AAH51649.1; -.
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PRINTS; PR01500; TROPOELASTIN.
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NCBI_TaxID=10116;
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                                                                                                            838
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                         ---GGLGVGGLGVPGVGGLGGIPPA 116
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                                                                                            Gaps
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE=88028442; PubMed=3665402; Sheppard P., Anderson N., Yeh H., Ornstein-Goldstein N., Indix Z., Sheppard P., Anderson N., Rosenbloom J.C., Citcila G., Yoon K., Rosenbloom J.; "Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.6%; Score 485; DB 2; Length 66:66.7%; Pred. No. 1.6e-19; ive 7; Mismatches 30; Indels
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Last annotation update)
                                                                           117 AAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFP
                                                                                                                                                                                                                                                                                  666 AA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence v
01-UTM-2003 (TrEMBLrel. 24, Last annotation
Elastin-CBEL3; NCBI gi: 163005 (Fragment).
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Coll. Relat. Res. 7:235-247(1987).
EMBL, M19372; AAA30501.1; -
EMBL, M1422; AAA30501.1; JOINED.
EMBL; M1946; AAA30501.1; JOINED.
EMBL; M19367; AAA30501.1; JOINED.
                                                                                                                                                                          -----GGACLGKACGRKRK 171
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   79 AAAKAAQFGLVGAAGL-----
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M19369; AAA30501.1;
M19370; AAA30501.1;
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M22773; AAA30501.1;
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M22775; AAA30501.1;
M22988; AAA30501.1;
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SEQUENCE OF 781-864 FROM N.A.

MEDINE=88330868; PubMed=2971041;

Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;

Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;

"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";

J. Biol. Chem. 263:13504-13507 (1988)

-!-FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-!-SUBUNIT: The Polyweric elastin chains are cross-linked together into an extensible 3D network.

-!- SUBCELLOLAR LOCATION: Extracellular matrix of elastic fibers.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat troppelastin mRNA revealed by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franzblau C., Pratt C.A., Faris B., Colannino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.;
"Role of tropoelastin fragmentation in elastogenesis in rat smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing, Named isoforms=8; Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=099372-6; Sequence=VSP_004245, VSP_004246;
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                                           628 GAGGLGVGGKPPKPFGGALGALGALGRGGACLGKSCGRKRK 666
---FPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rich C.B., Foster J.A.; "Characterization of rat heart tropoelastin.";
                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                     864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elastin precursor (Tropoelastin) (Fragment)
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IsoId=099372-3; Sequence=VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 268:551-55\overline{8}(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 29:9677-9683 (1990).
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                                                                                                                                                                                                                                                                         STANDARD;
       144 VAARPGFGLSPI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              782 PAAAAKAAKYGAAGLGGVL-GARPFPGGGVAARPGFGLSPIYPGGGAGGLGVGGKPPKPY 840
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Elastin.
By similarity.
By similarity.
7 and isoform 2, isoform 5, isoform 7 and isoform 8).
Frid=VSP_004244.
Missing (in isoform 3, isoform 5, isoform
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/FIId=vSp 004245.

Missing (in isoform 4, isoform 6, isoform 7 and isoform 8).
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                                             IsoId=Q99372-8; Sequence=VSP_004244, VSP_004245, VSP_004246;
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Alternative splicing; Connective tissue; Repeat; Signal;
              IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
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                                                         PTM: The crosslinks are made of deaminated Lys.
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Pred. No. 2.8e-19;
8; Mismatches 19;
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EMBL, J04035; AAA42268.1; --
EMBL, M86372; AAA42271.1; JOINED.
EMBL, M86355; AAA42271.1; JOINED.
EMBL, M86364; AAA42271.1; JOINED.
EMBL, M86364; AAA42271.1; JOINED.
EMBL, M86371; AAA42271.1; JOINED.
EMBL, M86371; AAA42271.1; JOINED.
EMBL, M86375; AAA42272.1; JOINED.
EMBL, M86375; AAA42272.1; JOINED.
EMBL, M86375; AAA42272.1; JOINED.
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mechan R.P.;

Brown P.L., Mechan L., Tisdale C., Mechan R.P.;

"The cysteine residues in the carboxy terminal domain of tropoelastin form an intrachain disulfide bond that stabilizes a loop structure and positively charged pocket.";

Biochem. Biophys. Res. Commun. 186:549-555(1992).

-I. FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-I. SUBGUIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-I. SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

-I. ALTERRATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-27 FROM N.A.
MEDLINE=91234332; PubMed=2031719;
Manohar A., Shi W., Anwar R.A.;
"Partial characterization of bovine elastin gene; comparison with the gene for human elastin.";
Biochem. Cell Biol. 69:185-192(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Nuchal ligament;
MEDLINE-89274159; PubMed-2543440;
Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing of elastin mRNA in the bovine nuchal ligament."; Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                                                                                                                                                                                               Raju K., Anwar R.A.;
"Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones.";
J. Biol. Chem. 262:5755-5762(1987).
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Alternative splicing; Connective tissue; Repeat; Signal;
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05-JUL-2004 (Rel. 44, Last annotation update) Elastin precursor (Tropoelastin).
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IsoId=P04985-2; Sequence=VSP_004239;
Name=3; Synonyms=C;
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IsoId=P04985-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                       MEDLINE=87194772; PubMed=3032943;
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                                                                                                Bos taurus (Bovine).
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                                                                        DR EMBL, M19372; AAA30500.1; -

EMBL, M19372; AAA30500.1; -

EMBL, M1936; AAA30500.1; -

DR EMBL, M1936; AAA30500.1; -

DR EMBL, M1936; AAA30500.1; JOINED.

EMBL, M1936; AAA30500.1; JOINED.

EMBL, M1936; AAA30500.1; JOINED.

REMBL, M1936; AAA30500.1; JOINED.

REMBL, M1936; AAA30500.1; JOINED.

REMBL, M19371; AAA30500.1; JOINED.

REMBL, M22771; AAA30500.1; JOINED.

REMBL, M22772; AAA30500.1; JOINED.

REMBL, M22773; AAA30500
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Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
Yen H., Ornstein-Goldstein N., Indik Z., Rosenbloom J.;

"Sequence variation of bovine elastin mRNA due to alternative
splicing.";

Coll. Relat. Res. 7:235-247(1987).

EMBL; M1922; AAA30499.1; --
EMBL; M1922, AAA30499.1; JOINED.

EMBL; M19366; AAA30499.1; JOINED.
Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.; "Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.7%; Score 442; DB 2; Length 679; 64.1%; Pred. No. 4e-17; ive 7; Mismatches 31; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.; "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               679 AA; 57652 MW; EB3C019E3BD7618D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBEL1; NCBI gi: 163003 (Fragment).
Bos tautus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.1
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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MEDLINE=85280426; PubMed=2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 747;
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MRS -> MG (in Ref. 2 and 3).

B -> G (in Ref. 2 and 3).

E 633C03E411643DB3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2).
/FTId=VSP 004239.
Missing (in isoform 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin.-CBEL2; NCBI gi: 163004 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 477; DB 1;
Pred. No. 4.8e-19;
7; Mismatches 31;
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                                       Elastin.
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SEQUENCE FROM N.A.
MEDLINE-88028442; PubMed=3665402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64229 MW;
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747 AA;
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NCBI_TaxID=9913;
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The polymeric elastin chains are cross-linked together
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InterPro; PR008160; Collagen.
LinterPro; IPR003979; tropoelastin.
Pfan; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                      EMBL; M18633; AAA48761.1; -.
                                                                                                                                                                                                                                                                                                                    EMBL; M21880; AAA49082.1; -.
EMBL; M15889; AAA49108.1; -.
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       SUBUNIT:
                                                                                              Name=1;
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      504 PGFGAVPGTLAAAKAAKFGPGGVGALGGVGDLGGAGIPGGVAGVGP-AAAAAAKAA 562
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                                                                                                                                                                                                                                                                                                                                                                                                                        597
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                                                                                                                                                                                                                                                                                                                             PSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                              Arch. Biochem. Biophys. 256:455-461(1987).
-!- FUNCTION: Major structural protein of tissues such as aorta and nuchai ligament, which must expand rapidly and recover completely.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87242320; PubMed=3593675;
Bressan G.M., Argos P., Stanley K.K.;
"Repeating structure of chick tropoelastin revealed by complementary
DNA cloning.";
                                        EMBL; M19371; AAA30499.1; JOINED.
EMBL; M22771; AAA30499.1; JOINED.
EMBL; M22773; AAA30499.1; JOINED.
EMBL; M22773; AAA30499.1; JOINED.
EMBL; M22775; AAA30499.1; JOINED.
EMBL; M22775; AAA30499.1; JOINED.
EMBL; M22775; AAA30499.1; JOINED.
EMBL; M23010; AAA30499.1; JOINED.
EMBL; M23010; AAA30499.1; JOINED.
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005579; C:extracellular matrix structural constituent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----FPGGACLGKACGRKRK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Aorta;
MEDLINE=87297534; PubMed=3502711;
Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
"Sequence analysis of elastin cDNA from chick aorta and tissuespecific transcription of the elastin gene in developing chick
                                                                                                                                                                                                                                                                       DB 2; Length 650;
                                                                                                                                                                                                                                                                                  Pred. No. 8.3e-17;
6; Mismatches 19; Indels
                                                                                                                                                                                                                                     650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         750 AA
                                                                                                                                                                                                                                                                    50.0%; Score 436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 85-750 FROM N.A. (ISOFORM MEDLINE=88309083; Pubmed=2841924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
                                                                                                                                                                                         InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
               AAA30499.1; JOINED.
AAA30499.1; JOINED
   AAA30499.1; JOINED
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SEQUENCE OF 457-750 FROM N.A.
                                                                                                                                                                                                                                                                                Local Similarity 55.5%;
tes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AARPGFGLSPI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    563 QF
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P07916;
                                                                                                                                                                                                                       NON TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01500; TROPOBLASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                   Name=2; Synonyms=Embryonic;
IsoId=P07916-2; Sequence=VSP 004241, VSP 004242;
-!- PTM: The crosslinks are made of deaminated Lys.
                                                                                     Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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8 X tandem repeats.
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 sofo	GVGVPC 004242	536 A -> G 571 G -> A 610 P -> A 654 A -> R 667 P -> R	33.9%; Score 295.5; DB 1; Length 750; larity 28.7%; Pred. No. 5.7e-09; Conservative 12; Mismatches 33; Indels 209; Gaps 12;	PRVPGAVPGVLGGLGALG57	: VPGVPGVPGVPGVPGVPGVGGPAAAAAAAAAAAAAAAAA	AAAAAAKAA 80	vpgvgvpgvpgvpgvgvpgvgvpgvgvpgvgvpgvgvp	GVPGVGGLGGIPPA	AKAAKYGAGGLAPGVGGLAPAVGGLAPGVGGLVPGVGGL-VPGVGGLAPGVGGLAPGVGA 5/4						VGVPGFGVSFIFPGGVGGQLGFGGKFPKIYGGALGALGFKGGVGCAQGKICGKKKK /50	STANDARD: PRT: 100 AA.	ימושקאדע (מושקאדע)	27.	4, Last annotation) (Fragment).		Chordata; Craniat	cetartiodactyla; kuminantia; Fecola; boyldae		PubMed=3839997;	Davidson J.M., Boyd C., May M., Luvalle F., Goldstein N., Smith J., Indik Z., Ross A., Golub E.,	gion of the sheep elasti	241:684-691(1965). ctural protein of tissues of must expand rapidly and	cross-linked	matrix of elastic finated Lys.	SWISS-PROT entry is copyright. It is produced through a collaboration been the Swiss Institute of Bloinformatics and the EMBL outstation
212	501	536 571 610 654 667 750 AA;	milarit	LPSTPSSPRVPG-	 PGVPGVP	t 1 1 1	PGVGVPG	AKAAQFGLVG	KAAKYGA		PGVGGPA	1 	GVGVLPG	AARPGFGLSPIFPG	GVPGFGV			(Rel.	004 (Rel. 4 (Tropoelast	, ;	(Sheep) Metazoa	Eutheria;	TaxID=9940;	FROM N.A.	Javidsor Joldstei	of the	CON: Ma	T: The	LULAR I	S-PROT che Swis
VARSPLIC	VARSPLIC	CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE	Query Match Best Local Similarity Matches 102; Conser	21 L	3 99 V	- 28	459 V		516 A	117 -	575 V		635 F		695 1	JLT 24 SHEEP FLS SHEEP	P11547:	01-OCT-1989	05-JUL-200 Elastin (7		Ovis aries Eukaryota;	Mammalıa; Caprinae;	NCBI_TaxII	NCE NE=8	Yoon K., Davidson J.M. Ornstein-Goldstein N.,	Rosenbloom J.; "Analysis of the 3' regi	Arch. Blochem -!- FUNCTION: nuchal lic	- ! - SUBUN	-!- SUBCE	This SWIS
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AAAGIVPGGPGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAKAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 AXAAQFGLVGAAGLGGL---------GVGGL----GVPGVG---GLGGIP---- 114
                                                                                                                                                                                                                                                                                                          86 FGL--VGAAGLGGLGVGGLG-VPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLG 142
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                                                                                                                                                                                                                                                                                                                              TISGUE-Whole embryo;

Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S., Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y., Sugano S., Isogai T.;

Nagahari K., Sugano S., Isogai T.;

Nagahari K., Sugano S., Isogai T.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO75494; BAC11651.1; ---

BR GO; GO:0005201; F:extracellular matrix; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R THEPPO; IPRO10451; Hexapep_transf.

R InterPro; IPRO10451; Hexapep_transf.

R InterPro; IPRO10451; Hexapep_transf.

R RINTS; PRO1161; HEXAPPE_TRANSFERASES; UNKNOWN_1.

PROSITE; PS001001; HEXAPPE_TRANSFERASES; UNKNOWN_1.

PROSITE; PRO1075 A72

NON TER 472

NON TER 472

SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF97IF3 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 280; DB 2; Length 472; 34.7%; Pred. No. 3e-08; ive 13; Mismatches 28; Indels 128;
                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                                                     Score 295; DB 1; Length 100
Pred. No. 1.5e-09;
5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     61 GGAGGLGVGGKPPKPFGGALGALGFPGGACLGKSCGRKRK 100
                                                                                                                                                                                    By similarity.
5C680C6A5AEE6786 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 GVAARPGFGLSPI-----FPGGACLGKACGRKRK 171
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01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0191.
Homo sapiens (Human)
                                                                                           EMBL; M26188; AAA31515.1; ALT_SEQ.
EMBL; M26189; AAA31516.1; -.
PIR; S59623; S59623.
Connective tissue; Repeat; Structural protein.
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100 AA; 8662 MW;
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Best Local Similarity 64.0%;
Matches 64; Conservative
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Best Local Similarity 34.7
Matches 90; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q6ZUN2
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231 SPEAQAAAAKAAKYGLVPGVGVAPGVGVAPGVGVAPGVGLAP--GVGVAPGVGVAPGVG 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AGQFPL-----GGVAARPGFGLS 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               supravalvular aortic stenosis.";
Hun. Mol. Genet. 6:1021-1028(1997).
EMBL; U93037; AAB65620.1;
EMBL; U93035; AAB65620.1; JOINED.
EMBL; U93035; Restracellular matrix; IEA.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001451; AAB656381in.
                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97358574; PubMed=9215670; MEDLINE-97358574; PubMed=9215670; Li D. X., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J., Morris C.A., Keating M.T.; "Elastin point mutations cause an obstructive vascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.4%; Score 273.5; DB 2; Length 602; 36.6%; Pred. No. 8.2e-08; ive 13; Mismatches 29; Indels 121.
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                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1
                                                                                                                                                                                                      602 AA.
                                                                                                                                                                                                                                               Created)
                                             ----IFPGG-ACLGKACGR 168
                                                                                    289 VAPGIGPGGVAAAAKSAAK 307
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                                                                                                                                                                                                                    015337;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 36.69
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EMBL; U93037; AAB65621.1; -.
EMBL; U93034; AAB65621.1; JOINED.
BMBL; U93036; AAB65621.1; JOINED.
GO; GO:0005201; C:extracellular matrix; IEA.
GO; GO:0005201; E:extracellular matrix structural constituent; IEA.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR001491; Hexapep transf.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PG00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                          MEDLINE=97358574; PubMed=9215670; Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J., Moris C.A., Keating M.T.; "Elastin point mutations cause an obstructive vascular disease, supravalvular aortic stenosis."; Hum. Mol. Genet. 6:1021-1028(1997).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Oshima A. Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
NNEDO human cDNA sequencing project.",
Submitted (UIL-2003) to the EMBL/GenBank/DDBJ databases.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR FLJ43523 fis, clone PLACES000282, weally similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
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                                                                                                                                                  64; Gaps
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Mammalia; Butheria; Primata; Catarrhini; Hominidae; Homo.
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Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK125511; BAC86188.1; -.
InterPro; IPR03979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;
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SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;
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30.8%; Score 269; DB 2;
Best Local Similarity 42.0%; Pred. No. 1.4e-07;
Matches 84; Conservative 12; Mismatches 40
                                                                                                                   30.8%; Score 269; DB 2; 42.0%; Pred. No. 1.4e-07;
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                                                                                                                                                      84; Conservative
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80 AAKAAQFGLV-------GAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAA 122
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                                                                                                                                                                                                                                                                                                                 Galleria mellonella (Wax moth).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bobotyota; Metazoa; Arthropoda; Hexapoda; Insecta; Ditrysia; Pyraloidea;
Pyralidae; Gallerianae; Galleria.
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TISSUB-POSTERIOR silk gland;

MEDLINE-22063145; PubMed=11886872;

Zurovec M., Sehnal F.,

"Unique molecular architecture of silk fibroin in the waxmoth,

"Unique molecular architecture of silk fibroin in the waxmoth,

"In lone. 277:22639-22647(2002).

EMBL, AF095239; AAG10393.1; -.

EMBL, AF095239; AAG10393.1; -.

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                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                 PRT; 1468 AA
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                                             421 SRSRRCPGSWHFPRSSGSSC 440
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01-OCT-2002 (TrEMBLrel. 22, La
Heavy-chain fibroin (Fragment)
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
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using sw model OM protein - protein search,

November 19, 2004, 15:19:20 ; Search time 37.3991 Seconds (without alignments) 1755.321 Million cell updates/sec on:

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935
1 AAAGLGAGIPGLGVGVGVPG......LSPIFPGGACLGKACGRKRK 183

Title: Perfect score:

Scoring table: Sequence:

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2002273 seqs, 358729299 residues Searched:

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Database:

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geneseqp2004s:* A_Geneseq_2 1: geneseqp 2: geneseqp 4: geneseqp 5: geneseqp 7: geneseqp 6: geneseqp 8: geneseqp Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SELPOK pr Protein p Protein p Protein p Protein p SELPSK po Plasmid p SELPOK po SELPOK

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VLGGLGALGGVGI PGGVVGAGPAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharamacutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELZ6-36 excluding exon 26A product
Aaw26346 SELP2 syn
Aaw53522 Amino aci
                                                                                                                                                                                                                                                               rropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a derivative or variant of human tropoelastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VLGGLGALGGVGIPGGVVGAGPAAAAAXKAAKKAQFGLVGAAGLGGLGVGGLGVFGCVPGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
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Best Local Similarity 100.0%; Pred. No. 3.2e-58;
Matches 183; Conservative 0; Mismatches 0;
                                                                 ALIGNMENTS
    AAW26346
AAW53522
                                                                                                                                              AAY01311 standard; protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 11; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0000B117.
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                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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281.5
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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated or subsequence has been miserted so that susceptibility to proteolysis is reduced susceptibility, and can be consequence has been inserted so that susceptibility, to proteolysis is increased. The derivatives have with reduced susceptibility, and can be consed where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative of derivatives, and other polypeptides containing tropoelastin derivative. The competitive inhibition of protease activity. The tropoelastin derivative derived protease-susceptibility sites, are useful in human or veterinary contained competition, particularly of smooth contains, as bulking agents and for inducing chemicatis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or protease cleavage site in tropoelastin contains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                         rropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
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                                                                                                                                                                                                                                           Amino acid sequence of a human tropoelastin derivative.
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Pred. No. 3.2e-58;
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                                                                                                                                AAY69138 standard; protein; 183 AA.
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Best Local Similarity 100.0%;
Matches 183; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-AU000580.
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                                                                                                                                                                                                             (first entry)
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KRK 183
                                    181 KRK 183
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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97AU-00008117.
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                                N-PSDB; ADE40133
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       Smithson G;
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                                    NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antisthatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzhaimer's; Parkinson's; asthma; fertility discret; vaccine; gene therapy; chromosome mapping;
                          GLGGIPPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
                                                                                                                         ADE40134 standard; protein; 692 AA.
                                                                                                                                                                              protein - SEQ ID 40.
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2001US-0313415P.
2001US-0313643P.
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2001US-0311979P.
2001US-0312892P.
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2001US-0322716P.
2001US-0323994P.
2001US-0340233P.
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2002US-0365478P.
2002US-0373814P.
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2001US-0310544P.
2001US-0310951P.
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2001US-0314466P.
2001US-0315403P.
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                                                                                                                                                           (first entry)
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23-AUG-2001;
28-AUG-2001;
                                                                                                                                                                             Human NOV16b
                                                                                                                                                           29-JAN-2004
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17-SEP-2001;
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05-FEB-2002;
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, ancrectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple aclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Purthemore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
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pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                       New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
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100.0%; Pred. No. 9.9e-58;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 40; 560pp; English
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Matches 183; Conservative
WPI; 2003-663472/62.
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New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
         (UNSY ) UNIV SYDNEY
                                                        WPI; 2000-182399/16
                                                                    N-PSDB; AAZ61144
                                                                                                     cell growth
                                Weiss AS;
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                                                                                                                                                                                    used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmacoutical, veterinary and cosmetic applications, e.g. as anti-products or hand lotions, also surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, despending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the synthetic human tropoelastin variant SHELGelta26A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tropoelastin, derivative; SHEL-delta-26a; SHEL; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer;
                                                                                                                                          tropoelastin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are
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                                                                                New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human reduced tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 935; DB 2; Length 698; 100.0%; Pred. No. 1e-57; cive 0; Mismatches 0; Indels (
                                                                                                                                           invention relates to a derivative or variant of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69069 standard; protein; 698 AA.
                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                      Claim 13; Fig 2; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-AU000580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98AU-00004723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth inhibition; peptidom metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                              WPI; 1999-132162/11
                 (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRK 698
                                                                                                                                                                                                                                                                                                 Sequence 698 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2000
                                                                                                                                                                                                                                                                                                                                              183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69069;
                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                        Query Match
                                         Weiss AS;
                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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The present sequence represents a human reduced tropoelastin derivative, consignated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin cerivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is reduced susceptibility, and can be concact with serum or wound exudate. The tropoelastin darives provide contact with serum or wound exudate. The tropoelastin derivatives competitive inhibition of protease activity. The tropoelastin derivative derived protease-susceptibility sites, are useful in human or veterinary contact indicting chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts osteocytes, chondrocytes and platelets. Condetivatives are competitive inhibitors of the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulibrilke growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 VLGGLGALGGVGIPGGVVGAGPAAAAAKAAKKAAGFGLVGAAGLGGLGVGGLGVPGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGGIPPAAAAKAGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 935; DB 3; Length 698; 100.0%; Pred. No. 1e-57; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease activity that causes blood clotting
Disclosure; Page 110-112; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO17360 standard; protein; 730 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRK 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 698 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human elastin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Homo sapiens

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The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a control sample. A reduced level is indicative of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin, transmembrane receptor PTK7, collagen type XVIII alpha 2, type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet derived growth factor receptor alpha, laminin M chain, subtilisin like protein PACS4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin
                                                                                                                                                                                                                 Winterhager E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAQFGLVGAAGLGGLGVGGLGVPGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                               Kreft B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 935; DB 5;
Pred. No. 1e-57;
; Mismatches 0;
                                                                                                                                                                                                               Kraetzschmar J,
 subtilisin like protein PACE4; nidogen
                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 15-16; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ19747 standard; protein; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                  21-AUG-2001; 2001EP-00250300.
                                                                                                                                                 25-SEP-2000; 2000DE-01048633
                                                                                                                                                                                                            Haendler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 183; Conservative
                                                                                                                                                                                                      Hess-Stumpp H, Haend
Regidor P, Scotti S;
                                                                                                                                                                                                                                                      WPI; 2002-317413/36.
                                                                                                                                                                             (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KRK 183
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                               Homo sapiens
                                                         EP1191107-A2
                                                                                      27-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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607 120 667

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667
                                                                                                                                                                                                                                                                Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAGIGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608 VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGCLGVPGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 935; DB 8; Length 730; 100.0%; Pred. No. 1e-57; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein of the invention SEQ ID NO:2477
                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 2566; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM03792 standard; protein; 663 AA.
                                                                                                                                                                                                      Zlotnik A;
                                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC
                                                                                                 26-NOV-2003; 2003WO-US038193
                                                                                                                                  26-NOV-2002; 2002US-0429739P
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                                                                                                                                                                                                     Ginsburg WM,
                                                                                                                                                                                                                                    WPI; 2004-441208/41
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                               WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KRK 183
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                                                                10-JUN-2004
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                                                                                                                                                                                                   Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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Homo sapiens,

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Sato H, Ishii S;
K, Irie R, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention may have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectide or as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM0159-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tropoelastin, hIE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 VIGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLGGI PPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG
                                                                                                                                                                                                                                                                                New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 927; DB 7; Length 663; Pred. No. 3.5e-57; 0; Mismatches 1; Indels
                                                                                                                                                                       Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tropoelastin derivative SHELdeltamodified.
                                                                                                                                                                                                                                                                                                                                                     claim 1; SEQ ID NO 2477; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY01303 standard; protein; 660 AA.
                                                                                                                                          (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
                                                                                                            22-MAR-2002; 2002JP-00137785
                                                                            12-APR-2002; 2002EP-00008400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.5
Matches 182; Conservative
                                                                                                                                                                            Sugiyama T,
                                                                                                                                                                                        Yamamoto J, Ĭsono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                         WPI; 2003-723558/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRK 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 663 AA;
                                                                                                                                                                                                                                                           N-PSDB; ADM01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1999
               EP1347046-A1
                                               24-SEP-2003
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                                                                                                                                                                            Esogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657
                                                                                                                                                                                                                                                                                              The invention relates to a derivative or variant of human tropoelastin (HTE) having elastin-like and/or macromolecule (specifically dycosaming)tycam (GAG)-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable GAG-binding properties, pedending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELdeltamodified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAGLGAGIPGILGVGVGVPGLGVGAGVPGFGAVPGFGAVPGALAAAKAAKYGAAVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKKG-AVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%; Score 920.5; DB 2; ilarity 99.5%; Pred. No. 9.9e-57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tropoelastin derivative SHEL26-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01310 standard; protein; 216 AA
                                                                                                                                                                                                                                                                           Claim 7; Fig 3; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRK 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 660 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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Homo sapiens

Homo sapiens

macromolecular binding properties, useful e.g. as surgical implants

New derivatives of human tropoelastin

WPI; 1999-132162/11. N-PSDB; AAX27705.

(UNSY) UNIV SYDNEY

Weiss AS;

18-JUL-1997;

98WO-AU000564 97AU-00008117

17-JUL-1998;

28-JAN-1999.

WO9903886-A1

Synthetic.

- with elastin-like or

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New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 107-109; 136pp; English.
           Location/Qualifiers
                                                                                                                                                             99WO-AU000580
                                         .504
                                                                                                                                                                                                                                                                                 2000-182399/16.
                                                                                                                                                                                                                      UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                               N-PSDB; AAZ61146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 731 AA;
                                                                                                 WO200004043-A1
                                     Cleavage-site
                                                     Cleavage-site
                                                                   Cleavage-site
                                                                                                                                                          19-JUL-1999;
                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                           cell growth.
                                                                                                                              27-JAN-2000
                                                                                                                                                                                                                                                    Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                               The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, peptide 26A, from hTE. The present c a bsence of a specific fragment, designated tropoelastin derivative SHEL26-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SSSQHLPSTPSSPRVPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AAKAAAKAAQFGLVGAAGLGGLGVGGLGVGGLGGLPPAAAKAAKYGAAGLGGVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRSLSPELREGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                         New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human tropoelastin splice form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AGQFPLGGVAARPGFGLSPIFFGGACLGKACGRKRK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 908.5; DB 2;
Pred. No. 2.6e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69068 standard; protein; 731 AA
                                                                                                                                                                                                                                                                                     Claim 35; Page 11; 82pp; English
                                                                                                                      97AU-00008117.
                                                                                         98WO-AU000564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%;
84.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 183; Conservative
                                                                                                                                                                                                              WPI; 1999-132162/11.
                                                                                                                                                  (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 216 AA;
                            WO9903886-A1
                                                                                      17-JUL-1998;
                                                           28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Synthetic.
                                                                                                                                                                               Weiss AS;
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The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence contained by the succeptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be consciplibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease cutivity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivatived protease-susceptibility sites, are useful continuary medicine, cosmetics (e.g. antiwrinkle or hand continually of smooth continually or subliking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition. particularly of smooth custoful for publishal or endothelial cells, fibroblasts, osteocytes, condrocytes and platelets. Peptidomimetics that mimic the protease conductive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or were also metastases, or to limit protease activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 SSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ------VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 908.5; DB 3; Length 731;
Pred. No. 7.5e-56;
0; Mismatches 0; Indels 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.2%;
84.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66657
ID AAB6
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The present invention relates to a minimal functional unit (MFU) of human elastin polypeptide. This protein is useful in a cosmetic material or a prosthetic material such as prosthesis for blood vessel replacements, for heart valve replacement, tissue replacement, for covering burns, for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; elastin; minimal functioning unit; MFU;
beta-sheet/beta-turn structure; fibrous protein; prosthesis;
blood vessel replacement; heart replacement valve; burn; wound; lamprin;
                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 SSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGLPPAAAAKAAKYGAAGLGGVLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.2%; Score 908.5; DB 4; Length 731;
84.7%; Pred. No. 7.5e-56;
ive 0; Mismatches 0; Indels 33;
                                                                                    Minimal function unit; MFU; human; elastin prosthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGLGAGI PGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 731
                                                                                                                                                                                                                                                                                                                Stahl R;
                                                       Human elastin protein without signal peptide
                                                                                                                                                                                                                                                                                                                 Rothstein S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU08725 standard; protein; 731
                                                                                                                                                                                                                                                                       PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human elastin mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 39pp; English.
                                                                                                                                                                                                                                          99US-00340736.
                                                                                                                                                                                                            29-JUN-2000; 2000WO-US017829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 covering wounds and stents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 84.7
Matches 183; Conservative
                            (first entry)
                                                                                                                                                                                                                                                                                   HSC RES & DEV LP
                                                                                                                                                                                                                                                                                                                     Keeley F,
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-102886/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 731 AA;
                                                                                                                                                     WO200100666-A2.
                                                                                                                                                                                                                                                                                                                     Rothstein A,
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                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                            29-JUN-1999;
                            05-APR-2001
                                                                                                                                                                                 04-JAN-2001
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AAB66657;
                                                                                                                                                                                                                                                                                       (HSCR-)
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The invention describes a polypeptide (1) comprising a minimal comprised of at least three beta-sheet/Deta-turn structures, and at and comprised of at least three beta-sheet/Deta-turn structures, and at least one amino acid residue that participates in cross-linking, and not least one amino acid residue that participates in cross-linking, and not construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel replacement, heart replacement valves and sheets for other uses such as proteins, for e.g. collagen, to provide prosthesis material that cresembles the natural structural materials of the body. MFUS modeled on resembles the natural structural materials of the body. MFUS modeled on lampin and other fibrous proteins e.g. spider silk, can be used to make contract a variety of materials, for a number of different applications, for e.g. in cords and ropes for use in parachutes and in cosmetics. Coating cynthetic prosthesis with MFUS modeled on human elastin significantly in cords in cords in parachutes and activation. The human-like MFU material is more biocompatible than other elastin containing materials. In contrast to solubilised fragments of elastin used before, an MFU is son.

Comparide of defined composition. The MFU is considerably smaller than the paractical purposes. Like other elastin preparations, the MFU is non-companied to manipulate for experimental and quantity, to handle in solution and to manipulate for experimental and quantity, to handle in structure, easier to produce or express in thrombogenic, thus providing a truly biocompatible materials and cher ribrous proteins expensed to make a variety of materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human cc elastin on which the MFU peptides of the invention are based
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDP 575
spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;
platelet activation inihibitor; non-thrombogenic; cell infiltration;
non-immunogenic; biocompatible; high tensile strength; elasticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not naturally occurring fibrous protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 731;
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                                                                                                                                                                                                                                                                                                                                                                        (HSCR-) HSC RES & DEV LP.
(PROT-) PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1B; 21pp; English.
                                                                                                                                                                                                                                                                                                           96US-0023522P
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Best Local Similarity 84.7
Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 731 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothstein A,
                                                                                                                                                                                                                                                                 29-JUN-1999;
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This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, metal or synthetic material, where the surface is coated with the naterial comprising the polypeptide, a cosmetic material comprising the polypeptide, a material comprising the polypeptide, a material comprising two or more polypeptides selected from (a) a polypeptide consisting essentially of a portion of the polypeptide comprising at least three beta sheet/beta turn structures, (b) a polypeptide consisting essentially of a particular comprising at least three beta turn amin acid sequence of an animal elastin comprising at least three beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
blood vessel; wound; burn healing; collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="region specifically claimed in claim 6"
188. .367
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/note= "region specifically claimed in claim 6"
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/note= "region specifically claimed
607. .717
                                                                                                                    AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                 ADL96420 standard; protein; 731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human elastin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 1B; 17pp; English.
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97US-00911364.
99US-00340736.
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
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07-AUG-1997;
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(ROTH/) 1
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sheets/beta turns, (c) a polypeptide consisting essentially of a portion of lamprin comprising at least three beta sheets/beta turns, and (d) a polypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, a polypeptide having the primary structure of a portion of a naturally occurring fibrous protein and a

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secondary structure comprising at least three beta sheets/beta turns, where each of the beta sheet/beta turn structures comprises from 3 to about 7 amino acids and the polypeptide is not a naturally occurring fibrous protein. The minimal functional unit (MFU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing. Alternatively the MFU can be co-aggregated with other proteins, for example collagen, to provide prosthesis material that resembles the natural structural materials of the body. The MFU based material is subject to infiltration of cells growing in the patient, including tissue replacement. The material is more biocompatible than other elastin containing materials proposed for prostheses.
                                                                                                                                                                                                                                                                                                                                                                                      576 SSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGUGILGGUVGAGPAAAAA 635
                                                                                                                                                                                                                                                                                                                                             575
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                                                                                                                                                                                                                                                                                                                             AAKAAAKAAQFGLVGAAGLGGLGVGGLGVGGLGGIPPAAAKAAKYGAAGLGGVLGG
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                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic polynucleotide(s) - encode recombinant tropoelastins and variants.
                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                              97.2%; Score 908.5; DB 7; Length 731; 84.7%; Pred. No. 7.5e-56; ive 0; Mismatches 0; Indels 33;
                                                                                                                                                                                                                                                                                                           1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tropoelastin; pharmaceutical; surgical dressing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic human tropoelastin (SHEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR56653 standard; protein; 733 AA.
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93AU-00009661.
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Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNSY ) UNIV SYDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-263633/32.
                                                                                                                                                                                                                 Sequence 731 AA;
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22-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weiss AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                 88
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                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                               577
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Human synthetic tropoelastin is susceptible to hydrolytic breakdown of the crosslinks. Such material may be useful in e.g. surgical applications, where the gradual loss of material over time is intended. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                    518 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRSLSPELREGDP
                                                                                                                                                                                                                                    -----VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAA
                                                                                                                                                                                                                                                                                            88 AAKAAAKAAQFGLYGAAGLGGGGGGGGGGGGGGGTPPAAAAKAAKYGAAGLGGVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                          Gaps
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                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derivatives of human tropoelastin - with elastin-like or
                                                                                                             Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of synthetic human tropoelastin SHEL.
                                                                                                                                          Indels
                                                                                                                                                                       1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                          Score 908.5; DB 2;
Pred. No. 7.5e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                         AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 733
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                                                                                                              97.2%;
84.7%;
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                                                                                                                                             Conservative
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                                                                                                                Query Match
Best Local Similarity
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                                                                                 Sequence 733 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
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                                                                                                                                           183;
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The present invention relates to the use of an agent that promotes elastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin elloymerisation, increasing F:G actin ratio in a smooth muscle cell, preventing or preventing obstructive vascular disease (e.g. restenosis), or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells is useful for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting
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                                                                                                                                                                                                                                                                                                                                    578 SSSQHLPSTPSSPRVPGALAAKAAKYGAAVPGVLGGLGGLGGVGIPGGVVGAGPAAAA 637
                                                                                                                                                                                                                                                                                                                 AAKAAAKAAQFGLVGAAGLGGGLGVPGVGGLGGLPPAAAAKAAKYGAAGLGGVLGG 147
                                                                                                                                                                                                                   577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL
                                                                                                                                                                                                      ----vpgalaaakaakygaavpgvlgglgalggvglpggvvgagpaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasctropic.
                                                                                                                                                    33;
                                                                                                                     Length 733;
                                                                                                                                                                                    AAAGLGAGI PGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA--
                                                                                                                     Score 908.5; DB 2;
Pred. No. 7.5e-56;
0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      148 AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                   AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 733
                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 138-141; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG75223 standard; protein; 757 AA
                                                                                                                     97.2%;
84.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2003; 2003WO-US009391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2002; 2002US-0368084P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tropoelastin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                         183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-833516/77.
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karnik S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003082203-A2.
                                                                                         Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2004
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                                                                                                                                                           Matches
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actin stress fiber formation or actin polymerization, increasing F:G actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis following angloplasty), or preventing stenosis. It is also useful in manufacturing a medicament for the treatment or prevention of occlusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease, arthritide, gene expression analysis, rheumatoid arthritis, collagen-induced, immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antinfilammatory, dermatological, immunomodulatory, lupus, ankylosing spondylitis, Fibrositis, fibromyalgia, osteoarthritis; gout, juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 SSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                   Length 757;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                                                                                             Score 908.5; DB 7;
Pred. No. 7.7e-56;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                             97.2%;
84.7%;
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.7
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thorton SL;
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                                                                                                                                                                                                                                              Sequence 757 AA;
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                                                                                                                                                                                         invention
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activities: immunosupressive, antitheumatic, antiarthritic, osteopathic, antigout, antinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
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            patient sample containing mRNA, analysing gene expression using the that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention utther comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; identification of other than a mouse, diagnosis of rheumatoid arthritis in a mammal other than a mouse, disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collageninduced arthritis; and reducing the symptoms associated with collageninduced arthritis; and reducing the symptoms associated with collageninduced arthritis; meaning the invention have the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The method comprises obtaining a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human elastin containing non-natural polypeptide MFU-1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unit; elastin; human; fibrous protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      722 AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 908.5; DB 7;
Pred. No. 7.7e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
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/note= "MFU-1 polypeptide"
autoimmune disease or arthritides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 97.2%; al Similarity 84.7%; 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 757 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFU-1; minimal
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97WO-CA000560

07-AUG-1997;

The invention relates to a novel method for diagnosing and analysing

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This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide c spider silk protein. The MFU polypeptides are self-aligning peptides having the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, wound or burn dressings, or stents. They can be used in cosmetic, elastic or high-tensile strength materials, e.g. ropes or parachute cord.

Prostheses based on the MFU allow penetration of endothelial cells, so the contract of the materials, and the MFU allow penetration of endothelial cells, so the contract of the materials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     become permanent, living, tissue replacemnts. The MFU polypeptides have better biocompatibility than known elastin-based materials. They are well defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombonomic and produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>AAKAAAKAAO</u>FGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------VPGALAAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA
                                                                                                                                                                                                                                New non-natural polypeptide with multiple beta-sheet, beta-turn structures - particularly based on human elastin, useful for coating prostheses, as wound dressings, etc., allows ingrowth of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 892; DB 2; Length 730;
Pred. No. 1.1e-54;
D: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                    Keeley FW, Rothstein SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB64761 standard; protein; 617 AA.
                                                                                  PROTEIN SPECIALTIES LTD.
HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 1B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.4%;
                                      97US-00911364.
                    96US-0023552P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                              WPI; 1998-145551/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 730 AA;
                                                                                                                                                       Rothstein A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            silk protein
                  07-AUG-1996;
07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                      PROT-)
                                                                                                           (HOSP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB64761
qq
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Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y; New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or (HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY. 28-MAR-2002; 2002EP-00007401. 25-JAN-2002; 2002US-00350978 05-NOV-2001; 2001JP-00379298 as targets of gene therapy Sugiyama T, J, Isono Y, Yoshikawa T, WPI; 2003-450961/43. N-PSDB; ADB62791 cancer; tumour. EP1308459-A2 famamoto J, 07-MAY-2003 Isogai T, Seki N,

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed its a polypeptide encoded by the polynucleotide or its patrial peptide, an antibody binding to the polypeptide or peptide or its patrial peptide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotide and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related confines for regulation of their expression and activity, or as targets effect the pense may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell capacity and genes related proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes. transcription related proteins, disease-related proteins and genes conciding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The CDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Claim 1; Page; 222pp; English

120 121 GLGGIPPAAAAKAAKGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180 453 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKKGAAVPG 61 VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG 0; Indels 18; Gaps Length 617; Score 822; DB 7; Pred. No. 7.4e-50; 0; Mismatches 87.9%; 90.2%; Matches 165; Conservative Query Match Best Local Similarity Sequence 617 AA; g δ q

European Patent Office.

695

575

Gaps

34;

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The present sequence represents a human elastin. Peptides derived from elastin are used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprising inhibiting the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cells in vivo, regulating the migration of smooth muscle cells in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized by diminished capacity to regulate smooth muscle cell function such as
     ----GVAARPGFGLSPIFPGGACLGKACGR 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                  Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAAGLGAGIPGLGVGVPVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 822; DB 3; Length 712;
Pred. No. 8.3e-50;
0; Mismatches 0; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                                                                                                                                                                                                                                   sequence of a human elastin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                        SVAS; hypertension; transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                          AAB08630 standard; peptide; 712 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 46; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00258217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000WO-US002526
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90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UTAH ) UNIV UTAH RES FOUND
 573 GLGGIPPAAAAKAAKY-
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                    KRK 183
                                                                       KRK 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200050068-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                              20-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keating MT,
                                                                                                                                                                                                                                                                 Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165;
                                    181
                                                                                                                                                                                           AAB08630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                      AABOB630
ID AABO
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The present sequence represents a fusion protein, comprising human elastin and c-myc, preceded by a His tag. The protein is used in compositions that are potent regulators of smooth muscle cell compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins of ragments of them) which have biological activities comprising: inhibiting the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cell in vivo; and regulating the migration of smooth muscle cell in vivo; and regulating the differentiation of smooth muscle cell in vivo; and regulating the differentiation of smooth muscle cell functions may be used the prophylaxis or treatment of a disorder characterized by attentions, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated and and and and and and activity or dissection.
                         ------GVAARPGFGLSPIFPGGACLGKACGR 709
                                                                                                                                                                                                                                                                                                                                                        Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  include SVAS (undefined), hypertension, and transplant arteriopathy
GLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                                                                                                                                                                                                                                                                                       Fusion protein comprising human elastin and c-myc.
                                                                                                                                                                                                          AAB08631 standard; peptide; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English,
                                     668 GLGGIPPAAAKAAKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00258217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000WO-US002526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 48; 79pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-533134/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li DY;
                                                                          KRK 183
                                                                                                                KRK 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200050068-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                 20-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                              AAB08631;
 121
                                                                          181
                                                                                                                                                                       RESULT 22
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1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGTGVGAGVPGFGAVPGALAAAKAAKYGAAVPG

87.9%; Score 822; DB 3; Length 730; 90.2%; Pred. No. 8.5e-50; ive 0; Mismatches 0; Indels :

Conservative

Matches 165;

61 VLGGLGALGGVGIPGGVVGAGPAAAAAKAAAKAAAKAAQFGLVGAAGLGGVGGLGVPGVG 120

g à 608 VLGGLGALGGVGIPGGVVGAGPAAAAAAKAAAKAAKAAQFGLVGAAGLGGLGVGGLGVPGVG 667

à

Query Match Best Local Similarity

Sequence 730 AA;

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WPI; 2003-663472/62.
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                pharmacogenomics
                                                                                                                                                                                                                                                                                       Sequence 711 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRK 711
     Guo X, Zhous
Guo X, Zhous
Edinger SR, Ell
                                                                  N-PSDB; ADE40131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1999
                                      Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                            667
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01305;
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Best Local S
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                                                                                                                                                                                                                                                   NOVX, cardiant; antiarteriosclerotic; hypotensive, cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypottension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
                                                                   GIGGIPPAAAAKYGAAGIGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180
                                                                                      718
             616
          557 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
                              61 VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAGFGLVGAAAGLGGLGVGGLGVPGVG
                                                617 VLGGLGALGGVGIPGGVVGAGPAAAAARAARAARAARAAGFGLVGAAGLGGLGVGGLGVPGVG
                                                                                    Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
                                                                                                                                                                             ADE40132 standard; protein; 711 AA.
                                                                                                                                                                                                                                     Human NOV16a protein - SEQ ID 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001, 2001US-0313643P.
20-AUG-2001, 2001US-0313643P.
21-AUG-2001, 2001US-0314466P.
28-AUG-2001, 2001US-0315853P.
29-AUG-2001, 2001US-0315853P.
21-SEP-2001, 2001US-032394P.
14-DEC-2001, 2001US-032394P.
14-DEC-2001, 2001US-0340233P.
05-FEB-2002, 2002US-0340233P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0312892P.
2001US-0313201P.
2001US-0313415P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-2002; 2002US-0365478P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373825P.
                                                                                           677 GLGGIPPAAAKAAKY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2002; 2002US-0373989P
                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2002; 2002WO-US024483.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                 tissue typing; human; NOV
                                                                                                             KRK 183
                                                                                                                              KRK 721
                                                                                                                                                                                                                                                                                                                                                     WO2003064589-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001;
17-AUG-2001;
17-AUG-2001;
20-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -2002;
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                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001;
03-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-2001;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                    29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003
                                                                                                                                                                                                 ADE40132;
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                                                                                                              181
                                                                                                                                                             RESULT 23
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, ancectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, notropic, antipabetic, immunosuppressive, anti-HIV, neuroprotective, notropic, antipatkinsonian, antiasthmatic and preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypotrension, cancer, obesity, diabetes, AIDS, multiple sclerosis graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the mucleic acids may be used as brother and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGGLGALGGVGIPGGVVGAGPAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                        or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAARAKYGAAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKAÇGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
   Anderson DW;
FL, Gorman L, Leite MW, Vernet CAM, Anderson Gerlach VL, Hjalt T, Rastelli L, Spytek KA; rman K, Malyankar UM, Macdougall JR, Stone DJ; jey DM, Burgess CE, Majumder K, Wolenc AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 819; DB 7;
Pred. No. 1.3e-49;
1; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 38; 560pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY01305 standard; protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.68;
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         K, Zhong M, Geill.
X, Zhong M, Geill.
SP. Ellerman K, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 164; Conservative
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The invention relates to a derivative or variant of human tropoelastin (ILTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybric proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, repebulds on presence or absence of a specific fragment, designated tropoelastin derivative SHELGamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tropoelastin, hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GALVGLGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaakaakygaavpgvi.gglgalggvgi.pggvvgagpaaaaaakaaakaagpglj.vgaagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AAAKAAKYGAAVEGVLGGLGALGGVGIPQCVVGAGPAAAAAAKAAAKAAQFGLVGAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 GCLGVGGLGGVPGVGGLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSP
                                                                                                                                                                                     New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 801; DB 2; Length 200; 82.2%; Pred. No. 8.3e-49; Live 1; Mismatches 10; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tropoelastin derivative SHELgamma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLGVGVGVPGLGVGAGVPGLGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY01304 standard; protein; 147
                                                                                                                                                                                                                                   Claim 15; Fig 8; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 IFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-AU000564.
                                             97AU-00008117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 82.2
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                       WPI; 1999-132162/11
                                                                         (UNSY ) UNIV SYDNEY
                                                                                                                                                         N-PSDB; AAX27707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 200 AA;
                                            18-JUL-1997;
                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1999
                                                                                                          Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY01304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 LVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKKAKYGAAGLGGVLGGAGQFPLGGVAAR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tropoelastin, derivative, proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation, growth inhibition, peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 GAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAKAAQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GGVPGALAAAKAGAAVFGVLGGLGALGGVC1PGGVVGAGPAAAAAAAAAAAAAAQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                         macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
                                                                                                                                                                             New derivatives of human tropoelastin - with elastin-like or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%; Score 729; DB 2;
99.3%; Pred. No. 7.1e-44;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 PGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 PGFGLSPIFPGGACLGKACGRKRK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY69137 standard; protein; 171 AA
                                                                                                                                                                                                                         Claim 19; Fig 7; 82pp; English.
              98WO-AU000564
                                            97AU-00008117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-AU000580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                 WPI; 1999-132162/11.
                                                                        SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                N-PSDB; AAX27706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200004043-A1
            17-JUL-1998;
                                          18-JUL-1997;
                                                                      AINO ( ASNO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY69137
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46 63

-- GVPGFGAVPGAL

Gaps

24;

Wang J; Wang Z;

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novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                     present sequence represents a human tropoelastin derivative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein (useful for identifying genetic disorders) #682
                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      157 AARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                    145 AARPGFGLSPIFPGGACLGKACGRKRK 171
                                                                        Disclosure; Page 133-134; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          ADE08527 standard; protein; 870 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                               77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                               Conservative
                                    WPI; 2000-182399/16
      (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 Sequence 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                               Matches 143;
                                                                                                                                                                                                                                                                                                                                         85
                      Weiss AS
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                     ADE08527
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GVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAAAAAAAGFG----LVGAAGLGGLGVGGLG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 VPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGG---A 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --RPPGPQGIPPAAAAKAAKAAKAGAAGLGGVLGGAGGFPLGGVAARPGFGLSPIFFGSELPV 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     673 ASPEDVAVPQPLHLALWQPCLARPTLSVAPEFLASCEQRWWEVEDSPRDPPTSRAGAAVP 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions, and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                           analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides, useful for expressing recombinant proteins for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKY-
                                                                                                                                                                                                                                       Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733 GVLGGLGALGGVGIPGGVVGAGPAAAAAAAAKAAAPFGEHWVEVGAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 685; DB 7; Length 870; 61.8%; Pred. No. 3.9e-40; ive 3; Mismatches 10; Indels
                                                                                                                                                                                                                       Goodrich RW, Ren F, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 1593; 1177pp; English.
                                                                                                                                                                                                                                                                 Weng G, Zh
Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE56670 standard; protein; 864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein Q99372, SEQ ID NO 2524
                                                                                                                                                                                                                                       Asundi V, Goodrich Ri
Xue AJ, Wehrman T, '
ng D, Chen R, Xu C,
              11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-0012858.
24-APR-2002; 2002US-0012858.
2001US-0339739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLGKACGRK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C--ASCGOR 847
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-569235/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 870 AA;
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADE07616
                                                                                                                                                                                                                                                                                          Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE56670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                   rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 3
                                                                                                                                                                                                                                                                     Ghosh M,
                                                                                                                                                                                                                                                                                               Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE56670
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                                                                                                                                                                                                                                                                                                                                contested the susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is conceased. The derivatives have with reduced susceptibility, and can be increased. The derivatives have with reduced susceptibility, and can be concerned to used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative provide competitive inhibition of protease activity. The tropoelastin derivative derived protease-susceptibility sites, are useful for proliferation.

The derivatives, and other polypeptides containing tropoelastin derivative and for inducing chemical for and for inducing chemicals. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or conductive inducing the protease cleavage site in tropoelastin cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin controlling localized growth of cancers or metastases, or to limit controlling localized growth of cancers or metastases, or to limit controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                               representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated
                                                                                                                                                            New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 OFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 PGFGAVPGALAAAKAGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 PSSPRVPGALAAAKAAKYGAAVPGVLGGLGGALGGVGIPGGVVGAGPAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 725; DB 3; Length 171; Pred. No. 1.5e-43;
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Gaps

82;

59

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

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799 VL-GARPFPGGGVAARPGFGLSPIYPGGGAGGLGVGGKPPKPYGGALGALGYQGGGCFGK 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The cDNA was sequenced from a clone prepd. from mRNA isolated from chicken acrta tissue. It can be used to produce tropoelastin which is a precursor of elastin which does not have desmosine, isodesmosine and lysynoyllensine residues and isn't cross-linked. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA fragment encoding trophy-elastin - has inhibiting activity towards platelet aggregation and is useful for prophylaxis of arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken; tropoelastin; platelet aggregation; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 294;
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rpt_unit= RU2:AAAAAKAAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3. .32
/label= repeat_region
/rpt_type= tandem
/rpt_unit= RU1:VPGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173. .182
/label= rpt_region
/rpt_type= tandem
/rpt_unit= RU1 (x2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                       AAP82484 standard; protein; 294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 5pp; Japanese.
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label= RU1
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                                                                                                                                                                                                                                                                                                  (revised)
                                                    177 ACGRKRK 183
                                                                                                 858 SCGRKRK 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                   Tropoelastin.
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                                                                                                                                                                                                                                                                                             24-OCT-2003
25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                        31-OCT-1990
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                                                                                                                                                                RESULT
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                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention discusses a composation comprising two or more isolated rate or human polymucolectides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also calaimed are a vector comprising the novel polymucleotide, a host cell which is differentially regulated in an animal subjected to pain and a that increases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition of one or more of the polymucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the compound that compound that regulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more of the sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the compound composition com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGLGAGVPGLGVGAGVPGFGAGAG--GFGAGAGVPGFGAGAVPGSLAASKAAKYGAAG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         680 GLGGPGGLGGPGGFGGPGGLGGVPGGVAGGAP-AAAAAAKAAKAAQYGLGGAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VPGVLGGLGALGGV-----GIPGGVVGAGPAAAAAAAAKAAKAAQFGLVGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GL------GGLGVGGLG----VPGVGGLGGIPPAAAKXAAKYGAAGLGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GGACLGK 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GAVPGALAAAKAAKYGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels 68; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGGF-
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59.1%; Pred. No. 5.5e-37;
ilve 9; Mismatches 24
                                                                                                                                                                                                                                                                                                                             Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 VLGGAGQFPLGGVAARPGFGLSPIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                               Befort K,
                                                                                                                            14-AUG-2002; 2002WO-US025765
                                                                                                                                                                     14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
                                                                                                                                                                                                                26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                           D'urso D,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-268312/26
Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 146; Conserv
                                    WO2003016475-A2.
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                                                                                   27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
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Matches
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This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be
                                                                                                                                                                                                                                                                                                                               GAGGLGAGVGVVGFTFPGGVGGQLGFGGKPPKTYGGALGALGFRGGVGCAQGKYCG 290
                        18;
                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                        -----ĠGLĠVĠĠLGVĠĠL 230
                                                                                                                                                                                                                                                                                                       179
                                                                                                                                      65 YGAGGIAPGVGGIAPGVGGIAPGVGGIAPGVGGIAPGVGG 124
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                                                                                      64
                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secretory proteins/membrane proteins, useful in
                                                     6 GAGIPGLGV-GVGVPGLGV-GAGVPGFGA---VPG----ALAAAKAAK
                                                                                 S GVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVPGTVPGAGPAAAKAAAKAAK

S GVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGTVPGAGPAAAKAAAKAAK

S GVGVPGVGVPGVGVPGVGVPGVFGVPGVFGVFGVPGVPGTVPGAGPAAAKAAAKAAKAAKAA
                                                                                                                                                                                -GVG-----GLGVPG
                                                                                                                                                                                                      ----GLGGIPPAAAKAAKYGAAGLGGV-LGGA
                                                                                                                                                                                                                                                                                                         ----GACLGKACG
                                                                                                                   --GALGGVG--IPG-----GVVGAGPAAA-----
                         140; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy or as candidate target molecules in drug development
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                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human membrane or secretory protein clone PSEC0191
                                                                                                                                                                                                                                                                        181 VGVLPGAGIPQVGVQPGRKPPKFGVPGAGVRGVGGIP----
Pred. No. 3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB88422 standard; protein; 472 AA.
                                                                                                                                                                                    - AAAAKAAAKAAQFGLVGAAGLGGL-
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                                                                                                                                                                                                                                                                                                            149 GOFPLGGVAARPGFGLSPIFPG
                             17;
                                                                                                                        54 YGAA--VPGV-----LGGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000EP-00114090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
              38.5%;
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                             117; Conservative
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                Best Local Similarity
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used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The proteins/membrane polypeptides antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists activity. The antibodies and also be used as therapeutic agents to used as diagnostic agents for activity. The antibodies and also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention, treatment and diagnosis of diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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nes 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 472 AA;
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" (gm2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep: *
" (gm2 6/ptodata/2/pubpaa/US07 NEW PUB.pep: *
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" (gm2 6/ptodata/2/pubpaa/US09 NEW PUB.pep: *
" (gm2 6/ptodata/2/pubpaa/US10 PUBCOMB.pep: *
" (gm2 6/ptodata/2/pubpaa/US10 NEW PUB.pep: *
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
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                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Land Ob contained	Semience 8 Appli	Semience 2477 An	Semiones 1	Semience 1, Appli	Company and	Semience 36, Appl	Semience 22 April	Semionee 23, Appl	ddy 'cz anience comiones 11 Appr	Somionee 21, Appl	Socionate 74, Appl	Sequence 24, Appl Sequence 26, Appl
SUMMARIES	ID	US-10-210-172-40	US-09-961-403-8	US-10-108-260A-2477	US-09-964-662-1	US-10-104-047-2915	US-10-210-172-38	US-08-806-029-36	US-10-441-965-23	US-08-806-029-25	US-10-441-965-21	US-10-096-986-74	US-08-806-029-34	US-10-117-931-26
	DB	15	10	15	10				15	α	15	14	80	14
	Query Match Length DB ID	692	730	663	731	617	711	969	969	750	969	1465	312	378
oje	Query Match	100.0	100.0	99.1	97.2	87.9	87.6	32.9	32.9	32.9	32.6	32.6	32.2	32.2
	Score	935	935	927	908.5	822	819	307.5	307.5	307.5	304.5	304.5	301.5	301.5
	Result No.	7	7	m	4	2	9	7	æ	6	10	11	12	13

	Sequence 52, Appl Sequence 53, Appl Sequence 53, Appl Sequence 33, Appl Sequence 34, Appl Sequence 40, Appl Sequence 40, Appl Sequence 62, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 25, Appl Sequence 36, Appl Sequence 4, Appl
B US-08-806-029-35 14 US-10-117-931-15 14 US-10-117-931-15 16 US-08-806-029-19 16 US-08-806-029-19 18 US-08-806-029-19 19 US-09-964-662-11 10 US-09-964-662-11 10 US-09-964-662-11 10 US-09-964-662-11 10 US-09-964-662-11 10 US-09-964-662-11 10 US-09-964-662-11 11 US-10-800-179-26 12 US-10-800-179-26 13 US-08-806-029-28 14 US-10-117-931-34 14 US-10-117-931-34 14 US-10-117-931-34 14 US-10-117-931-34 15 US-08-806-029-14 16 US-10-117-931-34 16 US-10-117-931-34 17 US-08-806-029-32 18 US-09-817-9694-31 18 US-09-841-321A-34 18 US-09-841-321A-34 18 US-09-841-321A-35 18 U	US-10-720-025-5 US-10-720-025-5 US-10-720-025-5 US-10-720-025-3 US-09-841-321A-4 US-09-841-321A-4 US-09-841-321A-4 US-09-837-9694-3 US-09-837-9694-3 US-09-837-9694-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-841-321A-3 US-09-861-597-6 US-09-861-597-6
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PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HE-STUMPP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: RABETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: REGIONS, PEDRO
APPLICANT: REGIONS, PEDRO
APPLICANT: SCOTTI, SINONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
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                                                                                                                                                                        Length 692;
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                                                                                                                                                                         100.0%; Score 935; DB 15; 100.0%; Pred. No. 2.8e-55;
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CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09961403
Publication No. US20030077589A1
GENERAL INFORMATION:
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SEQ ID NO 8
LENGTH: 730
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Best Local Similarity 100.
Matches 183; Conservative
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ORGANISM: Homo sapiens
                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 13, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 8, Appli
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Sequence 22, 1
Sequence 14, 1
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             US-10-720-025-23
US-10-720-025-24
US-10-720-025-42
US-10-720-022-55
US-08-806-029-13
US-09-837-969A-39
US-09-841-321A-39
US-09-861-597-8
US-10-414-760-13
US-10-414-760-13
US-10-414-760-24
US-10-414-760-24
US-10-720-025-60
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                                                                                                                                                                                                                                                                Sequence 40, Application US/10210172
Publication No. US20040043928A1
GENERAL INFORMATION:
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Padigaru, Muralidhara
Casman, Stacie
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APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
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Shimkets, Richard
Zerhusen, Bryan
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Voss, Edward
Boldog, Ferenc
Gorman, Linda
Leite, Mario
Vernet, Corine
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US-10-104-047-2915
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APPLICANT:
APPLICANT:
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Best Local 8
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668 GLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 727
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Sequence 1, Application US/09964662

Sequence 1, Application US/09964662

Sequence 1, Application US/09964662

Sequence 1, Application Wo. US20030166846A1

GENERAL INFORMATION:

APPLICANT: PROTEIN SPECIALITES LTD.

APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP

TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND

TITLE OF INVENTION: OTHER FIBROUS PROTEINS

FILE REFERENCE: 041082/0112

CURRENT FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: 09/340,/36

PRIOR PLLICATION NUMBER: 09/340,/36

NUMBER OF SEQ ID NOS: 11

SEQ ID NO: 11

SEQ ID NO: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 663;
                                                                                                                                             Sequence 2477, Application US/10108260A
Publication No. US2004005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILLE REPERENCE: H1-A0106
CURRENT APPLICATION UNMERR: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 54.58
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Pred. No. 9.3e-55;
0; Mismatches 1;
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SEQ ID NO 2477
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Best Local Similarity 99.5:
Matches 182; Conservative
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US-10-108-260A-2477
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; ORGANISM: Homo sapiens
US-09-964-662-1
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Best Local Similarity
                                                               728 KRK 730
                                  181 KRK 183
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US-10-108-260A-2477
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                                                                                        88 AAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG
                                                                --VPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA
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                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2915, Application US/10104047; Publication No. US20030236392A1; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA; CURRENT APPLICATION NUMBER: US/10/104,047; CURRENT FILING DATE:
; PRIOR PLING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696 AGQFPLGGVAARPGFGLSPIFFGGACLGKACGRKRK 731
                                                                                                                                                                                                                       148 AGOFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
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Publication No. US20040043928A1
GENERAL INFORMATION:
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Padigaru, Muralidhara
Casman, Stacie
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APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
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Shimkets, Richard
Zerhusen, Bryan
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; ORGANISM: Homo sapiens
US-10-104-047-2915
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TELEPHONE: (415) 781-1989
TELEPAX: (415) 388-249
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 amino acids
                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-806-029-36
                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 96; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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US-10-441-965-23
RESULT 7
US-08-806-029-36
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APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERENCE: 21402-416 A US 10/210/172
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR APPLICATION NUMBER: 60/309,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAQFGLVGAAGLGGLGVGGLGVPGVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GVAARPGFGLSPIFPGGACLGKACGR 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-04
PRIOR PLING DATE: 2001-08-07
PRIOR PLING DATE: 2001-08-07
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-15
PRIOR PLING DATE: 2001-08-16
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Pred. No. 1.8e-47;
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89.6%;
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
                                                                          Leite, Mario
Vernet, Corine
Anderson, David
Guo, Xiaojia
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Best Local Similarity 89.6
Matches 164; Conservative
                                     Boldog, Ferenc
Gorman, Linda
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; ORGANISM: Homo sapiens
US-10-210-172-38
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96 AQFGL--VGAAGLG--GLGVGGLGVPGVG--GLG----GIPPAAAAKYGA-AGLGGV 144
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Publication No. US20040014186A1
GENERAL INFORMATION
APPLICANT: KUMAR, MANO
TITLE OF INVENTION: SYNTHESIS OF INORGANIC STRUCTURES USING TEMPLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AGSGYGVPGYGYGYGYGYGYGYBGYGYBGYGYBGYGYBGYBGYBGABGSGAGAGSGAGAG 121
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Squeence 36, Application US/08806029

Publication No. US20020045567A1

GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Stedronsky, Erwin R.
TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.9%; Score 307.5; DB 8; ilarity 42.1%; Pred. No. 4.6e-13; Conservative 21; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 19, 2004, 16:06:25 ; Search time 8.231 Seconds (without alignments) 2139.188 Million cell updates/sec Run on:

US-09-743-818A-74 Title: Perfect score:

1 AAAGLGAGIPGLGVGVPG......LSPIFPGGACLGKACGRKRK 183 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 s

PIR 79:*
1. pir1:*
2. pir2:*
3. pir3:*
5. pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	111111111111111111111111111111111111111		elastin precuisor,	0		elastin precursor		millate	- 2	-			fibroin Chinoso	1.00	hypothetical glyci			hrmotherical glyci	4 -			hypothetical gryci		- (hypothetical glyci	4 -			hypothetical glyci
SUMMARIES	ID	EAHU	EABO	EAMS	\$59623	EART	A26601	QQBE31	A36068	E70895	A45560	B70812	E86179	T31328	E70824	F70806	F70573	G70917	E70917	C70720	A70812	D70807	A70770	B61615	E70806	F70963	D70878	A26099	A70989	F70824
	DB		Н	Н	~	Н	7	H	0	7	~	7	7	7	7	~1	0	N	1 7	N	0	N	~	7	~	~	~	7	~	7
	Length	792	747	860	770	864	784	641	718	167	907	882	212	2639	783	1901	479	741	1329	498	749	1489	603	268	1381	778	525	384	618	801
46	Query Match	7	71.9	70.3	70.1	68.4	40.9	28.3	26.0	24.8	24.2	23.1	22.9	22.8	22.7	22.7	22.6	22.6	22.6	22.5	22.4	22.4	22.2	22.1	22.0	22.0	21.9	21.8	H	21.8
	Score	908.5	672	S	655.5	640	382.5	26	•	m	226	216	214.5	213.5	212	212	211	211	211	210.5	209	209	207.5	207	206	205.5	205	203.5	203.5	203.5
	Result No.	Т	7	e.	4	വ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

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N; Contains: elastin precursor, splice form b; elastin precursor, splice form c c; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: A31865; A26728; G26728; A22343; 145886
R; Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams, Biochemistry 28, 2365-2370, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative sp. A,Reference number: A31865; MUID:89274159; PMID:2543440
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A; Residues: 1-27 < YEH>
A; Cross-references: UNIPROT: P04985; UNIPROT: Q28101; GB: J02855; NID: g340504; PIDN: AAA3077
K; Raju, K; Anwar, R.A.
J. Biol. Chem. 262, S755-5762, 1987
A; Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of A; Reference number: A92640; MUID: 87194772; PMID: 3032943
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A; Cross-references: GB: K03506; NID: 9163027; PIDN: AAA30506.1; PID: 9163028
A; Cross-references: GB: K03506; NID: 9163027; PIDN: AAA30506.1; PID: 9163028
B; Cicila, G; May, M; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbla Biochemistry 24, 3075-3080, 1985
A; Title: Structure of the 3' portion of the bovine elastin gene.
A; Reference number: A22343; MUD: 85280426; PMID: 2992576
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A;Residues: 613-747 <CIC>
A;Cross-references: GB:M20415
A;Rosenbloom, U.
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Blastin: Relation of protein and gene structure to disease
A;Reference number: 145885; MUID:85059254; PMID:6150137
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A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Rollecule type: DNA
A,Rollecule type: DNA
A,Rollecule type: DNA
A,Rollecule type: DNA
A,Cross-references: GB:M31898; NID:9163015; PIDN:AAA96417.1; PID:9163018
A,Cross-references: GB:M31898; NID:9243418, P.P.
Biochem: Biophys. Res. Commun: 186, 549-55, 1992
A,Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an interpretation and the carboxy terminal domain of tropoelastin form and A,Contents: annotation, disulfide bonds
C,Comment: The term tropoelastin refers to a soluble precursor form of the extracellula
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() Superfamily: elastin
() Superfami
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A;Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
A;Accession: B26728
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A; Cross-references: GB: K03505; NID: 9163025; PIDN: AAA30505.1; PID: 9163026
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A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
757 AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 792
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N;Alternate names: tropoelastin

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 22-Un-1990 Hesquence revision 26-Jul-1996 #text_change 09-Jul-2004

C;Date: 22-Un-1900 Hesquence revision 26-Jul-1996 #text_change 09-Jul-2004

C;Date: 22-Un-1900 Hesquence revision 26-Jul-1996 #text_change 09-Jul-2004

C;Date: 22-Un-1900 Hesquence revision 26-Jul-1996 #text_change 09-Jul-2004

R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, J.

R;Indik, Z.; Yeh, William elastin midicated by sequence analysis of classion: A3707

A;Reference number: A3707; MUID:87289668; PMID:3039501

A;Residues: 1-500,507-792 <IND>
A;Residues: 1-500,507-792 <IND>
A;Cross-references: UNIPROT:P1552; UNIPROT:Q9UMK5; GB:M16983; GB:J02948

A;Cross-references: UNIPROT:P1899

A;Cross-reference number: A33705; MUID:89255358; PMID:2722804

A;Reference number: A33705; MUID:89255358; PMID:2722804
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A; Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A; Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A; Note: this sequence represents a composite of several splice forms
A; Fazio, and J. ; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; the Lab. Invest. 58, 270-277, 1988
A; Title: Isolation and characterization of human elastin cDNAs, and age-associated varia A; Reference number: A53891; MUID:88156138; PMID:2831431
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A;Residues: 164-453,483-500,507-617,651-792 <FA2>
A;Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064
C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
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R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant A;Reference number: A30524; MUID:89009960; PMID:3171221
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A;Map position: 7q11.23-7q11.23
C;Superfamily: elastin
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A; Residues: 1-27 <BAS>
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MEDIJUBE-204588863; PubMed=11003705;
MATLINGALE D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
Duronio V., Koop B.F.;
"Comparative genomic sequence analysis of the Williams syndrome region
"LIMKL-RFC2) of human chronosome 7q11.23.";
Mamm. Genome 11:890-898(2000).
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Koop B.F., Tsui L.-C.;

"Identification of gene from a 500-kb region at 7q11.23 that is commonly deleted in Williams syndrome patients.";
                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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InterPro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
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Pred. No. 1.4e-41;
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Ol-APR-1990 (Rel. 14, Last sequence update)
Ol-JUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin).
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nes 183; Conservative
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Withou Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
"Isolated supravalvular aortic stenosis: functional haploinsufficiency
of the elastin gene as a result of nonsense-mediated decay.";
of the elastin gene as a result of nonsense-mediated decay.";
-!- FUNCTION: Major structural protein of tissues such as aorta and
nuchal ligament, which must expand rapidly and recover completely.
-!- SUBGUILLIA is polymeric elastin chains are cross-linked together
into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2; ISSO2-2; Sequence=VSP 004243; ISOid=15502-2; Sequence=VSP 004243; ISOid=15502-2; Sequence=VSP 004243; ISOid=15502-2; Sequence=VSP 004243; ISOid=15502-2; Sequence=VSP 004243; The crosslinks are made of deaminated Lys. DISEASE: Defects in BLN are a cause of autosomal dominant cutis laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder characterized by loose, hyperextensible skin with decreased characterized by loose, hyperextensible skin with decreased resilience and elasticity leading to a premature aged appearance. The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder diverticula, pulmonary artery stenosis and pyloric stenosis. DISEASE: Haploinsufficiency of ELN may be the cause of certain
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MEDLINE=96291399; PubMed=8689688;
Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green B.D.,
Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).

TISSUB=Skin fibroblast;

TISSUB=Skin fibroblast;

MEDLINE=89009560; PubMed=3171221;

Fazio M.J., Olsen D.R., Kauh B.A., Baldwin C.T., Indik Z.,

Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;

"Cloning of full-length elastin cDNAs from a human skin fibroblast
recombinant cDNA library: further elucidation of alternative splicing
utilizing exon-specific oligonucleotides.";

J. Invest. Dermatol. 91:458-464(1988).
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Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Rosenbloom J.C., Peltonen L., Rosenbloom J.; Atlernative splicing of human elastin mRNA indicated by sequence analysis of closed genomic and complementary DNA."; Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosenbloom J., Uitto J.; Intto J.; Isolation and characterization of human elastin cDNAs, and ageassociated variation in elastin gene expression in cultured skin
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"Cutis laxa arising from frameshift mutations in exon 30 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keating M.T.;
"LIM-kinasel hemizygosity implicated in impaired visuospatial
constructive cognition.";
Cell 86:55-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P15502-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVOLVEMENT IN CUTIS LAXA.
MEDLINE=99091639; PubMed=9873040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elastin gene (ELN).";
J. Biol. Chem. 274:981-986(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88156138; PubMed=2831431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibroblasts.";
Lab. Invest. 58:270-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 603-730 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVOLVEMENT IN SVAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.

DISEASE: Defects in ELN are the cause of supravalvular aortic stenoeis (SYAS) [MIM:48550] SYAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
GO; GO:0008203; P:cell proliferation; TAS.
GO; GO:000815; P:circulation; TAS.
GO; GO:0007887; P:crgnanogenesis; TAS.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
      cardiovascular and musculo-skeletal abnormalities observed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB06D15BA567AE46 CRC64;
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By similarity.

Missing (in isoform 2).

/FIId=VSP_004243.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M17282; AAC98394.1; ---
EMBL; M16983; AAC98394.1; ---
EMBL; M17265; AAC98394.1; JOINED.
EMBL; M17265; AAC98394.1; JOINED.
EMBL; M17265; AAC98394.1; JOINED.
EMBL; M17270; AAC98394.1; JOINED.
EMBL; M17271; AAC98394.1; JOINED.
EMBL; M17273; AAC98394.1; JOINED.
EMBL; M17273; AAC98394.1; JOINED.
EMBL; M17275; AAC98394.1; JOINED.
EMBL; M17276; AAC98394.1; JOINED.
EMBL; M17276; AAC98394.1; JOINED.
EMBL; M17276; AAC98394.1; JOINED.
EMBL; M17279; AAC98394.1; JOINED.
EMBL; M17280; AAC98394.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             730 AA; 63260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M36860; AAA52382.1; -- M24782; AAA53190.1; -- U62292; AAB17544.1; -- X15603; CAA33627.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A32707; EAHU.
HSSP; P50099; 12FJ.
Genew; HGNC:3327; ELN.
MIM; 130160; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X15603; CAA?
PIR; A32707; EAHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123700; -.
                                                                                                                                                                                                                                                         syndrome
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EMBL;
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MIM;
GO; GO;
GO; GO;
GO; GO;
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SOLITITIAN THE PRESENTATION OF THE PROPERTY OF
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VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLGVPGVG 120

61

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1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG

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461 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAANYGAAVPG 520
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                                                               668 GLGGIPPAAAKAAKYGAAGLGGVLGGAQQFPLGGVAARPGFGLSPIFPGGACLGKACGR
                                             121 GLGGIPPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S., Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y., Nagahari K., Sugano S., Isogai T., Subantited (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075554; BAC11696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR001379; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 643 AA; 55629 MW; FDFC042617F72A69 CRC64;
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%; Score 930; DB 2; Length 643; 99.5%; Pred. No. 4.6e-41; 1.1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
11-0CT-2002 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                643 AA
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01-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-MAR-2004 (TrEMBLrel. 26, La
Elastin.
Name=ELN;
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                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                        181 KRK 183
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Best Local S
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QBNB14;
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sapiens (Human)
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 SSSQHUPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDP 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------VPGALAAAKAGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M17281; AAC98395.1; JOINED.
GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
                                                                                                                             MEDINE-87274906; PubMed=3038460;
Indix Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
Rosenbloom J., Ornstein-Goldstein N.;
Rosenbloom J., Creston of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";
Connect. Tissue Res. 16:197-211(1987).
EMBL; M17283; AAC98395.1; JOINED.
EMBL; M17265; AAC98395.1; JOINED.
EMBL; M17265; AAC98395.1; JOINED.
EMBL; M17266; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                 MEDLINE=87289668; PubMed=3039501;
Indix Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.2%; Score 908.5; DB 2; Length 757;
84.7%; Pred. No. 6.7e-40;
ive 0; Mismatches 0; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
SEQUENCE 757 AA; 66136 WW; 23B7FE5B8AF85CA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AGOFFLGGVAARPGFGLSPIFPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR001451, Hexapep_transf.
InterPro, IPR003979, tropoelastin.
PRINTS, PR01500, TROPOELASTIN.
                                                                                                                                                                                                                                                                                                               JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                     EMBL, M17278; AAC98395.1; JOINED.
EMBL, M17279; AAC98395.1; JOINED.
EMBL, M17280; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                M17268, AAC98395.1; JOINED.
M17270; AAC98395.1; JOINED.
M17271; AAC98395.1; JOINED.
M17272; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                  M17276; AAC98395.1; JOINED. M17277; AAC98395.1; JOINED.
                                                                                                                                                                                                                                                                                                               M17273; AAC98395.1;
M17274; AAC98395.1;
M17275; AAC98395.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 84.7
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                         SEQUENCE FROM N.A.
                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
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EMBL;
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EMBL;
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05-JUL-2004 05-JUL-2004 05-JUL-2004

Hypothetical protein ELN. Name=ELN;

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RX 141

RX MEDLINE=22737999; PubMed=12853948;

RX Hiller LW. Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,

RA Hiller LW. Fulton R.S., Fulton L.A., Jaeger S., Walker R.,

RA Hiller LW. Fulton R.S., Fulton L.A., Jaeger S., Walker R.,

RA Wagner-McPherson C., Layman D., Maas J., Jaesh M.E.,

RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

RA Walle K., Delehaunty K.D., Miner T.L., Nash W.E., Cordan H.,

RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

RA Sun H., Bdwards J., Damar B., Courtney L., Kalicki J.,

RA Ozersky P., Bielicki L., Scott K., Holmes A., Harris A.,

RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

RA Strong C.M., Abbott A., Minx P., Maupin T., Rock S.M.,

RA Latrelle P., Miller N., Johnson D., Murray J., Woessner J.P.,

RA Hickenbotham A.M., Abbott A., Williag T., Rock E., Cook L.L.,

RA Hickenbotham M.T., Eddred J., Williams D., Bedell J.A., Mardis B.R.,

Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,

Clifton S.W., Clissoe S.L., Marra M.A., Kenber B.D., Ra Bailey J.A., McCher D., Clendenning J., Kaul R., Kent W.J., Furey T.S.,

RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,

RA Baddy S.R., McPherson J.D., Olson M.V., Bichler E.B., Green B.D.,

RRA Waterston R.H., Wilson R.K.;

RRA Waterston R.H., Wilson R.K.;

RRA Waterston R.H., Wilson R.K.;
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Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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84.7%; Pred. No. 6.7e-40;
ive 0; Mismatches 0; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001451; Hexapep_transf.
InterPro; IPR00379; tropoelastin.
PRINTS; PROISO0; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
HYPOTHERICal Protein. 2B24F955D8360738 CRC64; SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 183; Conservative
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                                                                       NCBI_TaxID=9606;
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AAS07435;
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02-MAR-2004 (
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ID AAS0
AC AAS0
DT 02-M
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WEDLINE-22737999; PubMed=12853948;

Wagner-McPherson C., Layman D., Mass J., Jasger S., Walker R.,

Wagner-McPherson C., Layman D., Mass J., Jasger S., Walker R.,

Wagner-McPherson C., Layman D., Mass J., Jasger S., Walker R.,

Wagner-McPherson C., Layman D., Mass J., Jasger S., Walker R.,

Wagner M., Becknon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

Rewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,

Sun H., Edwards J., Eradshaw-Cordum H., Ali J., Andrews S., Isak A.,

Nabrunt A., Nayyen C., Du F., Lamar B., Courtney L., Kalicki J.,

RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,

RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

RA Tin-Wollam A.M., Abbott A., Mins P., Maupin R., Strowmatt C.,

RA Latreile P., Miller N., Johnson D., Murray J., Woessner J.P.,

RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,

RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,

Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,

Raddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,

Waterston R.H., Wilson R.K.;

RA Nature 424:157-164(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Gaps
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.2%; Score 908.5; DB 2; Length 757; 84.7%; Pred. No. 6.7e-40; ive 0; Mismatches 0; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Du H., Rohlfing T., Strong C.;
"The sequence of Homo sapiens BAC clone CTB-51J22.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005056; AAS07435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66106 MW; 2B24F955D8360738 CRC64;
    27, Last annotation update)
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02-MAR-2004 (TrEMBLrel. 2
Hypothetical protein ELN.
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                                                             sapiens (Human).
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                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                  NCBI_TaxID=9606;
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Use Pauganue, Excus, Na., Aniobahara T., Goto Y., Hirao M., Shimizu F., Wakabe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Ite R., Otanki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., A Isono Y., Kawai-Hio Y., Saito K., Nishiswa T., Kimura K., Amashita H., Matsuo K., Nishiswa T., Kimura K., Wamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., B. Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Subinited (JUL-2003) to the EMBL/GenBank/DDBJ databases.

InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001451; Hexapep_transf.
InterPro; PR01500; TR0POpelastin.

PRINTS; PR01500; TR0POpelastin.

PROSITE; PR01010; HEXAPEP_TRANSFERASES; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAKAAQFGLVGAAGLGGLGVGGLGVPGVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GLGGIPPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGR 180
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
Irie R., Oteuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.9%; Score 822; DB 2; Length 570; 90.2%; Pred. No. 1.7e-35; live 0; Mismatches 0; Indels
                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last Sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein FLJ16246.
                                                                                   570 AA.
                                                                                                                                                (TrEMBLrel. 27, Created)
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165; Conservative
                                                                           PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Q6ZWJ6;
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    Takahashi-Fujii A., Oshima A.,
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
Indik Z., Yeh H., Ornstein-Goldstein M.;
Rosenbloom J.C., Peltonen L., Rosenbloom J.;
"Alternative splicing of human elastin mRNA indicated by sequence
analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                     18;
  Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (JUL-2003) to the EMEL/GenBank/DDBJ databases. EMBL, AK122731, BAC85506.1; -. SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;
                                                                                                                                                                 Length 570;
                                                                                                                                              Score 822; DB 2; Length 5),
Pred. No. 1.7e-35;
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Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
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Last annotation update)
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, M17277; AAC98393.1; U
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M17267; AAC98393.1;
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M17273; AAC98393.1;
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01-NOV-1996
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TISSUB-Human rectum tumor;

Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

BMBL, BS58199; CAD98665.1;

InterPro; IPR001451; Hexapep_transf.

PROSITE; PS00101; HEXAPEP_TRÂNSFERASES; UNKNOWN_1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GO, GO:0005578; C:extracellular matrix; NAS.
GO, GO:0030023; F:extracellular matrix constituent conferring.
InterPro; IPRO01451; Hexappe_transf.
InterPro; IPRO03973; tropoelastin.
PRINTS; PRO1500; TROPOELASTIN.
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89.6%; Pred. No. 3.1e-35;
.ive 0; Mismatches 1; Indels 1
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                                                                                                                 PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 687 AA; 59529 WW; 864068C4C8E9F88F CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686021208 (Fragment)
                                                                                                                                                                                   Score 822; DB 2; L
Pred. No. 1.9e-35;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 KRK 687
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH65566;
02-Mar-2004
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                                                                                                                                                                                                                                                                                                                             TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    909
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                                                                                                                                                                                                                                                                                                                                              TISSUE-Human fetal kidney;

TISSUE-Human fetal kidney;

POUSTAR A., Albert R., Moosnayer P., Schupp I., Wellenreuther R.,

Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BISSIA93910.1; -.

InterPro; IPR001451; Hexapep_transf.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 711 AA; 61765 MW; 95B624A99B4A98B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22388257; PubMed-12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhar N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazom...
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 815; DB 2; Length 71
Pred. No. 4.6e-35;
0; Mismatches 1; Indels
                                                                                                                                                (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                              711 AA
                                                                                                                                                                                                          Hypothetical protein DKFZp686F06102
Name=DKFZp686F06102;
                                                                                                            PRT;
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89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 164; Conservative
                                                                                                            PRELIMINARY;
                                                                                                                                            (TrEMBLre).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                01-OCT-2003
                                                                                                                                                                                         01-MAR-2004
                                                                                                                                                                      01-OCT-2003
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Name=ELN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                             07Z3F5;
                                                                                                      Q7Z3F5
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                                                               RESULT 11
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                                                                                     Q7Z3F5
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180
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., "Gener B.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Gener than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGGI PPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPI FPGGACLGKACGR
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1500; TROPOBLASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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Pred. No. 4.9e-35;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2004) to the EMBL/Geni
EMBL; BC065566; AAH65566.1; -
InterPro; IPR001451; Hexapep transf.
InterPro; IPR003979; tropoelastin.
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MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
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AAA30498.1;
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Coll. Relat.
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EMBL;
EMBL;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 814; DB 2; Length 65
89.6%; Pred. No. 4.9e-35;
ive 0; Mismatches 1; Indels
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submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC065566; ARH65566.1; -.
SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin; NCBI gi: 163002 (Fragment).
                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Coll. Relat. Res. 7:235-247(1987).
EMBL; M1932; AAA30498.1; -.
EMBL; M1422; AAA30498.1; JOINED.
EMBL; M19366, AAAA30498.1; JOINED.
EMBL; M1936; AAA30498.1; JOINED.
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SEQUENCE FROM N.A.
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Best Local Similarity
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562 ALGGVGDLGGAGIPGGVAGVGP-AAAAAAKAAKAAQFGL---GGVGGLGVGGLGAVPGA 617
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REMBL; M19371; AAA30498.1; JOINED.
REMBL; M22771; AAA30498.1; JOINED.
REMBL; M22773; AAA30498.1; JOINED.
REMBL; M22774; AAA30498.1; JOINED.
REMBL; M22774; AAA30498.1; JOINED.
REMBL; M22774; AAA30498.1; JOINED.
REMBL; M22774; AAA30498.1; JOINED.
REMBL; M22784; AAA30498.1; JOINED.
REMBL; M22988; AAA30498.1; JOINED.
REMBL; M23010; AAA30498.1; JOINED.
REMBL; M23010; AAA30498.1; JOINED.
REMBL; M23010; REATTACEILUlar matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
RICHEPPO; IPR003979; tropoelastin.
RENITS; PR01500; TROPOELASTIN.
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MEDLINE=88028442; PubMed=3665402;
Yeb H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
"Sequence variation of bovine elastin mRNA due to alternative
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
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MEDLINE=85280426; PubMed=2992576;
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M19372; AAA30501.1; -.
M11422; AAA30501.1; JOINED.
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M19367; AAA30501.1; U
M19368; AAA30501.1; U
M19369; AAA30501.1; U
M19370; AAA30501.1; U
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747 AA;
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                                                                                                                                                                       VLGGLGALGGVGI PGGVVGAGPAAAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLG-VPGV
                                                                                                                                                                                                                                               120 GGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPI-----F
                                                                                                                                                16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91234332; Pubmed=2031719;
Manchar A., Shi W., Anwar R.A.;
"Partial characterization of bovine elastin gene; comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kosenbloom J.,
"Structure of the bovine elastin gene and S1 nuclease analysis of
alternative splicing of elastin mRNA in the bovine nuchal ligament.";
Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Nuchal ligament;
MEDLINE=89274159; PubMed=2543440;
Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.
                                                             GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raju K., Anwar R.A.;
"Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones.";
J. Biol. Chem. 262:5755-5762(1987).
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                           72.9%; Score 682; DB 2; Length 666; 73.3%; Pred. No. 3.5e-28;
                                                                                                                                              28; Indels
                                                                                                          666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;
                                                                                                                                                                                                                                                                                                                                ELS BOVIN STANDARD; PRT; 747 AA. P04985; P04986; P04987; Q29421; 13-Aug-1987 (Rel. 05, Created) 24UG-1987 (Rel. 05, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Elastin precursor (Tropoelastin).
                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene for human elastin.";
Biochem. Cell Biol. 69:185-192(1991).
EMBL; M19371; AAA30501.1; JOINED.
EMBL; M22771; AAA30501.1; JOINED.
EMBL; M22772; AAA30501.1; JOINED.
EMBL; M22774; AAA30501.1; JOINED.
EMBL; M22774; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
EMBL; M22775; AAA30501.1; JOINED.
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MEDLINE=87194772; PubMed=3032943;
                                                                                                                                                                                                                                                                                  169 PGGACLGKACGRKRK 183
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                                                                                                                                          Matches 143; Conservative
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NCBI_TaxID=9913;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb.sib.ch).
                                                           Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
"The cysteine residues in the carboxy terminal domain of tropoelastin form an intrachain disulfide bond that stabilizes a loop structure and positively charged pocket.";
                                                                                                                                           Biochem. Biophys. Res. Commun. 186:549-555(1992).
-!- FUNCTION: Major Structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
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MRS -> MAG (in Ref. 2 and 3).

E -> G (in Ref. 2 and 3).

633C03E411643D83 CRC64;
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Alternative splicing; Connective tissue; Repeat; Signal;
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Missing (in isoform 2).
/FIId=VSP_004239.
Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                      Name=3; Synonyms=C;
IsoId=P04985-3; Sequence=VSP 004240;
-!- PIM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                           Name=1; Synonyms=A;
IsoId=P04985-1; Sequence=Displayed;
Name=2; Synonyms=B;
IsoId=P04985-2; Sequence=VSP_004239;
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[4]
DISULFIDE BOND.
MEDLINE=92337651; PubMed=1632791;
midline=92337651; PubMed=1632791;
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InterPro; IPR003979; tropoelastin.
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EMBL; K03505; AAA30505.1; -.
EMBL; K03506; AAA30506.1; -.
EMBL; J02855; AAA30776.1; -.
EMBL; M58652; AAA03519.2; -.
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                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617
                                                                                                                                                                                                                                                                                732
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                                                                                                                       919
                                                                                                                                                               119
                                                                                                                                                                                            617 ALGGVGDLGGAGIPGGVAGVVP-AAAAAKAAAKAAKAQFGL---GGVGGLGVGGLGAVPGA 672
                                                                                                                                                                                                                                         120 GGLGGIPPAAAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPI-----F 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GAVPGALAAA 49
                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 KAAKYGAA------VPGVLGGLGALGGVGIPGGVVGAG-PAAAAAAAAAQF
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                                                                                                                                                             61 VLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLG-VPGV
                                                                                                                                                                                                                                                                              673 VGLGGVSPAAAKAAKFGAAGLGGVLGAGQPFPIGGGAGGLGVGGKPPKPFGGALGALGF
                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPG
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green E.D.;
Submitted (ULL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR289665; AAF99336.1; -.
GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003799; tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                           16;
      Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                             30;
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57.1%; Pred. No. 7.8e-27;
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      Score 663; DB 1;
Pred. No. 3.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
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Matches 145; Conservative
        70.9%;
                                                                                                                                                                                                                                                                                                                              PGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                 PGGACLGKSCGRKRK 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
ELN (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACLGKACGRKRK 183
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                            Similarity
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NCBI_TaxID=10090;
                                                   Matches 141;
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          Query Match
Best Local &
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Q9ESZ9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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O
                                                                                                                                                                                                                                                                     STRAIN=BALB/C; TISSUE=Lung;
MEDLINE=95130069; PubMed=7829060;
MYGHOF KS., Sechler J.L., Boyd C.D., Passmore H.C.;
"Uge of an intron polymorphism to localize the tropoelastin gene t
mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
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OCOBESAAE1EDD7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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57.1%; Pred. No. 8.1e-27;
tive 9; Mismatches 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connective tissue; Repeat; Signal; Structural
                                     34, Created)
34, Last sequence update)
44, Last annotation update)
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860 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; AS5721; EAMS.
MGD; MGI:95317; Eln.
InterPro; IPR003979; tropoelastin.
                                                                                                          Elastin precursor (Tropoelastin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71955 MW;
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GGGCFGKSCGRKRK 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 145; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860
855
                                                                                                                                                    Mus musculus (Mouse).
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                                                                                    (Rel.
                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                      05-JUL-2004
                                            01-OCT-1996
                                                                  01-OCT-1996
  ELS MOUSE
P54320;
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                                                                                                                                    Name=Eln;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=20530913: PubMed=11076861;

MEDLINE=20530913: PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yamanoto R., Inoue K., Togawa Y., Itawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Nacazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRANT=CS7BL/6J; TISSUB=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1830(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTRAIN-CSTBL/6J; TISSUE-Thymus;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Hayashida K., Handoka T., Hirancho K., Hirancka T., Hirozane T., Horis J., Inchi Y., Itoh M., Kagawa I., Kantawa T., Kordo S., Konno H., Kawai J., Kojima Y., Kondo S., Konno H., Kawai J., Kojima Y., Kondo S., Konno H., Kawai J., Kojima T., Kondo S., Konno H., Kawai J., Kojima T., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Satich H., Sakai C., Sakai K., Sahazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last sanotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched (Blastin, clone:A630042119 product:elastin, full insert sequence
                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                   860 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                             (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium,
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SEQUENCE FROM N.A.
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                                                                                                                 01-MAR-2003
                                                                                                                                                                                                                                                                                                                          Name=Eln;
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Q8C9L8

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DT Q8C9L8

DT 01-MAR-1

DT 01-MAR-1

DT 01-MAR-1

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ALTAINTER 1971 No. 1122 DEFENDMENT C. 31, STATULE 2018 NO. 1122 DEFENDMENT C. 31. TATULE STATULE STATU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGLGVGGLGVPGVGGLGGIPPAAAKAAKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:95317; Eln.
GO; GO:0007519; P:myogenesis; IMP.
GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
GO; GO:0043149; P:stress fiber formation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71938 MW; 7C340F2FFFDC92E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 GAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFP----
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01-OCT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 AA
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                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; IISSUE=Manmary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
SEQUENCE 860 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
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099372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88330868; PubMed=2971041;
MEDLINE-88330868; PubMed=2971041;
MEDLINE-88330868; PubMed=2971041;
MEDLINE-88330868; PubMed=2971041;

"Rat tropoclastin is synthesized from a 3.5-kilobase mRNA.";

J. Biol. Chem. 263:13504-13507(1988).

-! FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.

-! SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-! SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-! ALTERNATIVE PRODUCTS:
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=099372-8; Sequence=VSP 004244, VSP_004245, VSP_004246; -!- PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               smooth
                                                                                                                                                                                                                                                                                                                                                                                                             Franzblau C., Fratt C.A., Faris B., Colannino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.; "Role of tropoelastin fragmentation in elastogenesis in rat smoor muscle cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=299372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q99372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
                                                                                                                                                                                                                                                                               PubMed=2913947;
Rich C.B., Foster J.A.;
"Characterization of rat heart tropoelastin.";
Arch. Biochem. Biophys. 268:551-558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q99372-4; Sequence=VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q99372-2; Sequence=VSP_004244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q99372-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 264:15115-15119(1989).
                                                                                                                                                                                                                Biochemistry 29:9677-9683 (1990)
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 22-31 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 12:651-658(1992).
                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A.
                            Rattus norvegicus (Rat)
                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2768256;
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---VPGVLGGLGALGGV-----GIPGGVVGAGPAAAAAAAAAAAAAQFGLVGAA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSP 004245.
Missing (In isoform 4, isoform 6, isoform 7 and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                By similarity.
Missing (in isoform 2, isoform 5, isoform 7 and isoform 8)
/FIId=VSP_004244.
                                                                                                                                                                                                                                                                                                                                                                                                                                       isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGF--GAVPGALAAAKAAKYGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBEL1; NOEI gi: 163003 (Fragment).
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 3, isoform 5, 6 and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                        PRINTS, PRO1500, TROPOELASTIN.
Alternative splicing, Connective tissue, Repeat, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456894BB09E79FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 640; DB 1;
Pred. No. 6.2e-26;
9; Mismatches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 004246
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                                                                                                                                                                                                                                                                                                                             By similarity.
                              EMBL; M86372; AAA42271.1; DINED. EMBL; M86355; AAA42271.1; JOINED. EMBL; M86363; AAA42271.1; JOINED. EMBL; M86364; AAA42271.1; JOINED. EMBL; M86371; AAA42271.1; JOINED. EMBL; M86371; AAA42271.1; JOINED. EMBL; M86373; AAA42272.1; JOINED. EMBL; M86375; AAA42272.1; JOINED. EMBL; M86375; AAA42272.1; JOINED. EMBL; M86375; AAA42272.1; JOINED.
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                                                                                                                                                                                                                                       IPR003979; tropoelastin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.4%;
59.1%;
               AAA42268.1;
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864
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                                                                                                                                                                                                                                                                                               Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         864 AA;
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Best Local Similarity
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NCBI_TaxID=9913;
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22
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263
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M60647;
J04035;
                                                                                                                                                                                                      PIR; A36106;
RGD; 67394; I
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                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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us-09-743-818a-74.rup

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Biochemistry 24:3075-3080(1985)
                         [2]
SEQUENCE FROM N.A.
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                                                                                                                     splicing.";
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P07916;
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Best Local (
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                                                                                                                                                               DR ENBL; National Coll. Relat. Res. 7:235-247(1997).

ENBL; M19372; AAA33499.1; -...

ENBL; M19366; AAA33499.1; -...

ENBL; M19366; AAA33499.1; JOINED.

ENBL; M19369; AAA33499.1; JOINED.

ENBL; M19370; AAA33499.1; JOINED.

ENBL; M19371; AAA33499.1; JOINED.

ENBL; M19371; AAA33499.1; JOINED.

ENBL; M22772; AAA33499.1; JOINED.

ENBL; M22773; AAA33499.1; JOINED.

ENBL; M22773; AAA33499.1; JOINED.

ENBL; M22773; AAA33499.1; JOINED.

ENBL; M22773; AAA33499.1; JOINED.

ENBL; M22775; AAA33499.1; JOINED.

ENBL; M22785; Extracellular matrix; IEA.

TO GO:0005201; F:extracellular matrix structural constituent; IEA.

ENDL; ENDL; ENDLSOU; TROPOELASTIN.

TO NOW TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Gaps
                                                                                        MEDLINE=88028442; PubMed=1665402; Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.; "Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Elastin-CBEL2, NCBI gi: 163004 (Fragment).
Bus taurus (Bovine) 163004 (Fragment).
Bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S., Yeh H.;3., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.; "Structure of the 3' portion of the bovine elastin gene."; Biochemistry 24:3075-3080(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE-85280426; PubMed-2992576;
Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
"Structure of the 3' portion of the bovine elastin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.7%; Score 633; DB 2; Length 650; 63.6%; Pred. No. 1.2e-25; ive 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GLGGIPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 ALGGVGDLGGAGIPGGVAGVGP-AAAAAAKAAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                          splicing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GGLGGIPPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPI------F 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 ALGGVGDLGGAGIPGGVAGVGP-AAAAAKAAAKAAKAAQFGL---GGVGGLGVGGLGAVPGA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 VGLGGVSPAAAAKAAKFGAAGLGGVLGAGQPFPIGGGAGGLGVGGKPFKPFGGALGALGF 664
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87242320; PubMed=3593675;
Bressan G.M., Argos P., Stanley K.K.;
"Repeating structure of chick tropoelastin revealed by complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005578; C:extracellular matrix; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
MEDLINE=88028442; PubMed=3665402; Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N., Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.; "Sequence variation of bovine elastin mRNA due to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 AAAGLPAGVPGLGVGVPGLGVGVGVPGLGVGAGVPGFGAGPGGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.6%; Score 622.5; DB 2; Length 68.2%; Pred. No. 4.3e-25; Indels iive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER 1 1 1
SEQÜENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
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SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2)
                                                                                                                 Coll. Relat. Res. 7:235-247 (1987).
EMBL; M1972; AAA30500.1; -
EMBL; M1942; AAA30500.1; -
EMBL; M1946; AAA30500.1; JOINED.
EMBL; M19366; AAA30500.1; JOINED.
EMBL; M19369; AAA30500.1; JOINED.
EMBL; M19370; AAA30500.1; JOINED.
EMBL; M19370; AAA30500.1; JOINED.
EMBL; M19371; AAA30500.1; JOINED.
EMBL; M22771; AAA30500.1; JOINED.
EMBL; M22771; AAA30500.1; JOINED.
                                                                                                                                                                                                                                        EMBL, M19368; AAA30500.1; JOINED. EMBL, M19369; AAA30500.1; JOINED. EMBL, M19370; AAA30500.1; JOINED. EMBL, M22771; AAA30500.1; JOINED. EMBL, M22772; AAA30500.1; JOINED. EMBL, M22772; AAA30500.1; JOINED. EMBL, M22774; AAA30500.1; JOINED. EMBL, M22774; AAA30500.1; JOINED. EMBL, M2278; AAA30500.1; JOINED. EMBL, M22988; AAA30500.1; JOINED.
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Biochemistry 26:1497-1503(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 PGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 68.2
133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken)
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63697 MW;
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Matches 118; Conservative
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427
431
513
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667
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571
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                                                                                                                                                                              Arch. Biochem. Biophys. 256:455-461(1987).

-!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-!- SUBUNIT: The polyweric elastin chains are cross-linked together into an extensible 3D network.
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                         Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T., "Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcription of the elastin gene in developing chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF01391; Collagen; 1.
PRINTS; PR01500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                  Name=2: Synonyms=Embryonic;
Isold=P07916-2; Sequence=VSP 004241, VSP 004242;
PTM: The crosslinks are made of deaminated Lys.
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5...
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8. similarity.
By similarity.
Allysine (Potential).
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    MEDLINE=88309083; PubMed=2841924;
Baule V.J., Foster J.A.;
"Multiple chick tropoelastin mRNAs.";
Biochem. Biophys. Res. Commun. 154:1054-1060(1988)
                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elastin.
8 X tandem repeats
                                                                                                                                                                                                                                                                                                                                        Isold=P07916-1; Sequence=Displayed;
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InterPro; IPR008160; Collagen.
InterPro; IPR003979; tropoelastin.
                                                                                                              MEDLINE=87297534; PubMed=3502711;
                                                                                 SEQUENCE OF 457-750 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M18633; AAA48761.1; -.
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581 PAAAAKAAAKYAAKYG----AGVGGVPGAVPGAVPGVPGVPGVTPGVGGVPSLVPGVGVPG 636
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Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
Ota T., Nishikawa T., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075494; BAC11651.1; --
EMBL; Oc.0005578; C:extracellular matrix; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 YGAA--VPGV-----LGGL----GALGGVG--IPG-----GVVGAGPAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 -PGFGLSPIFPG------GACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 VPGFGVSPIFPGGVGGQLGFGGKPPKTYGGALGALGFRGGVGCAQGKYCGRKRK 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                     -> GLGGFGGQQPGVPLGYPIKAPKLPG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                    /FILESOST COTTON
/FTIGEVSP 004242.
A -> G (in Ref. 3).
A -> A (in Ref. 3).
P -> R (in Ref. 3).
P -> R (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 382; DB 1; Length 750;
Pred. No. 1.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E57ECD60C6EE556F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein PSEC0191.
                                        (Potential) (Potential)
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/FTId=VSP 004241.
G -> GVGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -AAAAKAAAKAAQFGLVGAAGLGGL-----
                   Allysine (Allysine Allysine G -> GLGG
Allysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                            Elastin (Fragment)
                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
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Best Local &
                                                                  015336
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                                             RESULT 26
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                                                          015336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LGGLGALGGV----GIP--GGVVGA 80
                                                                                                                                         1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAGAAVPG
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GPAAAAAAAAAAAAAQFGLVGAAGLGGLGVGGLG-VPGVGGLGGIP----PA----AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAGLGAGIPGLGVG-VGVPGLGV-GAGVPGLGV----GAGVPGFGAVPG-----ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Elastin point mutations cause an obstructive vascular disease, supravalvular acrtic stenosis.";
Hum. Mol. Genet. 6:1021-1028 (1997).
EMBL; U33034; AAB65620.1; -...
EMBL; U33034; AAB65620.1; JOINED.
EMBL; U33036; AAB65620.1; JOINED.
GO: GO:0005578; C:extracellular matrix; IEA.
GO: GO:0005578; C:extracellular matrix; IEA.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AKAAKYGAAGLGGVLGGAGOPPLGGVAARPGFGLSP---IFPGGACLGKACG 179
                                                                                                                          .;
0
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46.1%; Pred. No. 4.6e-11;
tive 18; Mismatches 46; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97358574; PubMed=9215670;
Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
Morris C.A., Keating M.T.;
                                                                                                 Length 472;
                                                                     472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51807 MW; 53B5B9A71EF04807 CRC64;
                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                  PRINTS; PRO1500; TROPOELASTIN.

PROSTTE; PSO1101; HEXAPEP_TRANSFERASES; UNKNOWN_1.

NON TER

SEQUENCE 472 A4, 42265 MW; 8D7A0F3A9FF971F3 CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001451; Hexapep transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
                                                                                               Score 365; DB 2;
Pred. No. 7.8e-12;
0; Mismatches 1;
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                                                                                               39.0%;
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                        376 VLGGLGALGGVGI 388
                                                                                                                                                                                         61 VLGGLGALGGVGI 73
                                                                                                                   72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 6
602 AA;
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 107; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Elastin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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SEQUENCE
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81 GPAAAAAAAAAAAAAAGFGLVGAAGLGGLGVGGLG-VPGVGGLGGIP----PA----AA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------EGGLGALGGV----GIP--GGVVGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGLGAGIPGLGVG-VGVPGLGV-GAGVPGLGV----GAGVPGFGAVPG-----ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mol. Genet. 6:1021-1028(1997).

EMBL; U93034; AAB65621.1; -10.

EMBL; U93034; AAB65621.1; JOINED.

EMBL; U93036; AAB65621.1; JOINED.

EMBL; U93056; AAB65621.1; JOINED.

GO; GO:0005278; C:extracellular matrix; IEA.

GO; GO:0005201; E:extracellular matrix structural constituent; IEA.

InterPro; IPR001451; Hexapep transf.

InterPro; IPR001451; Hexapep transf.

InterPro; DENGOS CO:0005201
467 AKAAQFALLINLAGLVPGVGVAP--GVGVAPGVGVAPGVGLAPG----VGVAPG 513
                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 AKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSP---IFPGGACLGKACG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97358574; PubMed=9215670; Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J., Morris C.A., Keating M.T.; Blastin point mutations cause an obstructive vascular disease, supravalvular aortic stenosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 635;
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72950C364127B2A4 CRC64;
                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1500, TROPOBLASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.6%; Score 351.5; DB 2
46.1%; Pred. No. 4.7e-11;
tive 18; Mismatches 46
                                                                                                                 635 AA
                                                                                                                                                            Created)
                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 AAKAAKYGAAVPGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein FLJ43523.
Homo sapiens (Human).
                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107; Conservative
                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 AA;
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SEQUENCE FROM N.A.
TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                                                                                                               --GIPPA-------AAAKAAKYGA---AGLGGV--LG-GAGQFP-----LG 154
                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Saito M., Kimura K., Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Nabo human cDNA sequencing project."; Sugiyama J., Isogai T.; Nabo human cDNA sequencing project."; Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Suganato S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Sumit d (JUL-2003) to the BMEL/GenBank/DDBJ databases.

EMBL, AXI25511, BAC86188.1; -
                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ43523 fis, clone PLACE5000282, weakly similar to Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
                                                                                                                                                                                                                                                       --GVGVP-----GLGVGAGVPG
                                                                                                                                                                                                                                                                                 174 APGVGGAFAĞIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGYGPG-GVAĞ
                                                                                                                                                                                                                                                                                                              30 LGVGAGVP---GFGAVPGALAAAK-AAKYGAAVPGVLGGLGALGGVGIP----GGVVG
                                                                                                                                                                                                                                                                                                                              233 AAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPGVGGAGVPGVPGNIPGIGGIAG
                                                                                                                                                                                                                                                                                                                                                                        80 AGPAAAAAAKAAAQFGLVGAAGL-----GGLGVGGLGVFGVG--GLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101;
                                                                                                                                                                                                                           Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.9%; Score 307.5; DB 2; Length 559; 39.6%; Pred. No. 8.3e-09; ive 14; Mismatches 48; Indels 101.
                                                                                                                                                                                             32.9%; Score 307.5; DB 2; Length 39.6%; Pred. No. 8.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559 AA; 53787 MW; 20938FFEC5492A01 CRC64;
                                                                                                                                                                 53787 MW; 20938FFEC5492A01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Meteria, Crimiata, Vertebrata, Mammalia, Butheria, Primata, Catarrhini, Hominidae, Mammalia, Eutheria, Primata, Catarrhini, Hominidae,
                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVAGVPGVGGSRSRRCPGSWHFPRSSGSSC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---PIFPGGAC 173
                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                        2 AAGLG---AGIPGLGV----
                                                                                                                                                           PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK125511; BAC86188.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.9
Best Local Similarity 39.6
Matches 107; Conservative
                                                                                                                                                                                                                                Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVAARPGFGLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                         559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC86188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        124
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                                                                                                                                                                       SEQUENCE
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                                                                                                                                                      80 AGFAAAAAAAAKAAQFGLVGAAGL-----GGLGVGGLGVPGVG--GLG---- 123
                                                                                                                                                                                                                                                                                                             351 GAĞİPGAAVPGVVSPEAAAKAAKAAKYGARPGVĞVĞĞIPTYĞVĞAĞGFPGFFGVGVGGIP 410
174 APGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLFGGYGLPYTTGKLPYGYGPG-GVAG 232
                                                                                                   233 AAGKAĞYPTGTĞVĞPQAAAAAAAAKFĞAĞAAĞVLPĞVĞĞAĞVPĞVPĞAIPGIĞĞIAĞ 292
                                                                                                                                                                                                                                                               -----IG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 VGTPAAAAAAAAAAKAAKKG--AAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGTPVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                   30 LGVGAGVP---GFGAVPGALAAAK-AAKYGAAVPGVLGGLGALGGVGIP-----GGVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch Biochem. Biophys. 241:684-691(1985).

Arch Biochem. Biophys. 241:684-691(1985).

-i- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completel.

-i- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.

-i- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

-i- PTM: The crosslinks are made of deaminated Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                  AAAKAAKYGA---AGLGGV--LG-GAGQFP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the 3' region of the sheep elastin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 GVAARPGFGLSPI------FPGGACLGKACGRKRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y similarity.
5C680C6A5AEE6786 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=8530573; PubMed=3839997;
MEDLINE=85305763 J.M., Boyd C., May M., Luvalle P.,
Ornstein-Goldstein N., Smith J., Indik Z., Ross A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 295; DB 1;
Pred, No. 1.3e-08;
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Connective tissue; Repeat; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                           411 GVAGVPGVGGSRSRRCPGSWHFPRSSGSSC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA
                                                                                                                                                                                                                                                                                                                                                                           ------PIFPGGAC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elastin (Tropoelastin) (Fragment)
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01-OCT-1989 (Rel. 12, Last seq
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100 AA; 8662 MW;
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nes 64; Conserv
                                                                                                                                                                                                                                                                          124 --GIPPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9940;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AGPAAAAAAAAAAAAAAQFGLV------GAAGLGGLGVGGLGVPGVGGL 122
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                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 12, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
11-Independent (TremBlrel. 22, Last annotation update)
11-Independent (TremBlrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 GGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.5%; Score 266.5; DB 2; Length 1468; Best Local Similarity 35.6%; Pred. No. 2e-06; Matches 83; Conservative 23; Mismatches 58; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 AGVPGFGAVP--GALAAAKAAKYGAAVPGV----LGGLGALGGVGIPG----
61 GGAGGLGVGGKPPKPFGGALGALGFPGGACLGKSCGRKRK 100
                                                                                                                                                                                             PRT; 1468 AA
                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                           RESULT 30
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Sequence 4, Appli Sequence 4, Appli Sequence 9096, Ap Sequence 22139, Sequence 353761, Sequence 353761, Sequence 368385, Sequence 368385, Sequence 353760, Sequence 353770, Sequence 353770, Sequence 353770, Sequence 123914,

Sequence 8462, Ap Sequence 1250, A Sequence 17360, A Sequence 14639, A Sequence 1970, Ap Sequence 1618, Ap Sequence 1618, Ap Sequence 138437, Sequence 138437, Sequence 153020,

Sequence 164333, Sequence 193612, Sequence 267711, Sequence 397, App Sequence 56899, A

4 US-10-369-493-19907 3 US-10-0424-599-1966 5 US-10-424-599-20451 US-10-425-115-340008 6 US-10-425-115-340008 6 US-10-425-115-340008 6 US-10-425-115-340008 6 US-10-425-115-323761 US-10-425-115-323761 US-10-425-115-323761 US-10-425-115-323761 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 6 US-10-425-115-333770 7 US-10-425-115-33370 8 US-10-128-128-6589 9 US-10-128-128-6899 1 US-10-369-493-17360 1 US-10-369-493-17360 1 US-10-369-493-15744 1 US-10-369-493-15744 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-493-184-32 1 US-10-369-184-32 1 US-10-369-184-32 1 US-10-369-184-32 1 US-10-378-626-5090 1 US-10-378-626-5090 1 US-10-437-963-11648-99 1 US-10-437-963-11648-

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Sequence 1, Appli
Sequence 38, Appl
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Sequence 9, Appli
Sequence 10, Appli
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Sequence 2477, Ap
Sequence 40, Appl
Sequence 8, Appli
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11, Appl
2, Appli
122700,
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Sequence 1
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1: \cgn2_6/ptodata/2/pubpaa/NEOT_BW PUB.pep:*

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US-09-964-662-1
US-10-210-172-38
US-10-210-172-38
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Maximum Match 100%
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                                     protein search, using
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Sequence 95, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 303, App Sequence 303, App Sequence 16176, A Sequence 15794, A Sequence 15794, A Sequence 201970, Sequence 6076, Ap

Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl

Sequence 196197, Sequence 5090, Ap Sequence 356194, Sequence 45940, A

Sequence Sequence Sequence Sequence

126058, 177048, 74310, A 66102, 168409,

Sequence

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US-10-210-172-40
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                             Sequence 7961, Ap
Sequence 167410,
Sequence 254505,
Sequence 135427,
Sequence 13589, A
Sequence 6, Appli
Sequence 20, Appli
                                                                                                                                                               Sequence 1441, Ap
Sequence 1270, Ap
Sequence 74026, A
Sequence 680, App
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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 15; Length 663; 100.0%; Pred. No. 0.048; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0%; Score 59; DB 14; Length 617; Best Local Similarity 100.0%; Pred. No. 0.045; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                           RESULT 1
US-10-104-047-2915
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: US20030236392A1e1 full length cDNA
; FILE REFERRINCE: H1-A0105
; CURRENT FILING DATE: 2002-03-25
; CURRENT FILING DATE: 2002-03-25
; RIOR FILING DATE:
; NUMBER: OF SEQ ID NOS: 4096
; SOFTWARE: PARENTIN Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
6 US-10-437-963-196404
6 US-10-437-963-177050
4 US-10-156-761-791050
6 US-10-437-963-177050
7 US-10-425-115-254505
6 US-10-425-135-34547
US-09-815-242-13588
5 US-10-386-050A-6
5 US-10-386-050A-6
5 US-10-386-050A-6
5 US-10-389-566-1441
5 US-10-389-566-1441
5 US-10-389-266-1441
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-108-260A-2477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
     US-10-108-260A-2477
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 711
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US-09-964-662-1

i Gequence 1, Application US/09964662

j Sequence 1, Application US/09964662

j General INFORMATION:

APPLICANT: PROTEIN SELEIALITES LTD.

APPLICANT: PROTEIN SELEIALITES LTD.

TITLE OF INVENTION: SELEIALITES MODELED ON HUMAN ELASTIN AND TITLE OF INVENTION: OTHER PIBROUS PROTEINS

TITLE OF INVENTION: OTHER PIBROUS PROTEINS

TITLE OF APPLICATION NUMBER: US/09/964,662

CURRENT APPLICATION NUMBER: US/09/964,662

CURRENT FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PATENTIN VOIL: 2.1
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APPLICANT: HESTUMPP, HOLGER
APPLICANT: HESTUMPP, HOLGER
APPLICANT: HESTUMPP, HOLGER
APPLICANT: KRETZSCHARA, JOERN
APPLICANT: KRETZ, BERTHOLT
APPLICANT: KRETJ, BERTHOLT
APPLICANT: REGION, PEDRO
APPLICANT: SCOTIL, SIMONE
ITILE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
ITILE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE PATENTIN Ver: 2.1
ISBQ ID NO 8
LENGTH: 730
INVESTINE PRIME PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTINE PATENTI
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Pred. No. 0.054;
Mismatches 0; Indels (
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                                                                                                                                                                                                                                                Sequence 8, Application US/09961403
Publication No. US20030077589A1
GENERAL INFORMATION:
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              1 ALAAAKAAKYGAA 13
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Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-10-210-172-38
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LENGTH: 731
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APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
FILE REFERENCE: 21402-416 A
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PRIOR PLILAGATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR PLILAGATION NUMBER: 60/373,814
PRIOR PLILAGE DATE: 2001-09-21
PRIOR PLILAGE DATE: 2001-04-09
PRIOR PLILAGE DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PLILAGATION NUMBER: 60/310,544
PRIOR PLILAGATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-09
PRIOR PLILAGATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PRILAGATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-17
PRIOR PRILAGATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
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Pred. No. 0.18;
1; Mismatches
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CURRENT FILING DATE: 2001-08-01
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PRIOR APPLICATION NUMBER: 60/309,501
                                                                                                                                                                                                                                                                                 Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
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Malyankar, Uriel
MacDougall, John
Stone, David
Alsobrook II, John
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Zerhusen, Bryan
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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591 ALAARRAAKYGAA 603
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Gorman, Linda
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Vernet, Corine
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fi, Weizhen
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ORGANISM: Homo sapiens
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US-09-964-662-11
; Sequence 11, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICATON NO. USECIALITIES LTD.
; APPLICANT: PROTEIN SPECIALITIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041068/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PARENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2. Application US/09964662
| Sequence 2. Application US/09964662
| Publication No. US20030166846A1
| GENERAL INFORMATION:
| APPLICANT: PROTEIN SPECTALTIES LTD.
| APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
| TITLE OF INVENTION: SILE-ALIGHTNG PREPTIDES MODELED ON HUMAN ELASTIN AND TITLE OF INVENTION: OTHER FIRROUS PROTEINS
| FILE REPERRENCE: 041082/0112
| CURRENT APPLICATION NUMBER: US/09/964,662
| CURRENT APPLICATION NUMBER: US/09/964,662
| PRIOR FILING DATE: 1999-06-29
     APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND TITLE OF INVENTION: OTHER FIBROUS PROTEINS FILE REFERENCE: 041082/0112 CURRENT APPLICATION NUMBER: US/09/964,662 CURRENT FILING DATE: 2003-05-08 PRIOR PAPLICATION NUMBER: 09/340,736 PRIOR FILING DATE: 1999-06-29 NUMBER OF SEQ ID NOS: 11 SSEQ ID NOS: 11 SSEQ ID NO 10 LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
APPLICANT: PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                78.0%;
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 90.9
Matches 10; Conservative
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ORGANISM: Homo sapiens
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US-09-964-662-10
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Best Local Similarity
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US-09-964-662-2
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                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: And Vibra
APPLICANT: And Vibra
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENGINE OF SEQ ID NOS: 285684
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Publication No. US20030166846A1
GENERAL INFORMATION:
APPLICANT: PROTIENT SPECIALTIES LTD.
APPLICANT: PROTIEN SPECIALTIES LTD.
APPLICANT: PROTIEN SPECIALTIES LTD.
APPLICANT: PROTIEN SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND TITLE OF INVENTION: OTHER FIBROUS PROTIENS
FILLE SEPERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT APPLICATION NUMBER: 09/340,736
PRIOR PILLING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 11
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US-10-424-599-269890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsuze
LOCATION: (1)..(144)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                            ; Sequence 269890, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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US-09-964-662-10
Sequence 10, Application US/09964662
Publication No. US20030166846A1
GENERAL INFORMATION:
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90.9%;
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SEQ ID NO 9
LENGTH: 117
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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Best Local Similarity
                                                             US-10-424-599-269890
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US-09-964-662-9
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Gaps

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
GURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-22
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-29
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16900
LENGTH: 485
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                                                                                                                        Score 40; DB 14; Length 378;
Pred. No. 65;
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Pred. No. 89;
                                                                                                                                                                              2; Indels
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                                                                                                                                                   Pred. No. 65;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16900, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                      ORGANISM: Chloroflexus aurantiacus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%;
75.0%;
                                                                                                                             67.8%;
75.0%;
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72.7%;
                                                                                                    Query Match
Best Local Similarity 75.0
                                                                                                                                                                                                                                                                       292 LAARALVYGAA 303
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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US-10-369-493-19927
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                                                                            US-10-369-493-9086
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            LENGTH: 378
TYPE: PRT
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US-10-47-963-122700

Sequence 122700, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: APPLICANT: Application Value

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

SEQ ID NO 122700

SEQ ID NO 122700

LEAR TITLE OF END TO 122700

SEQ ID NO 122700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9086, Application US/10369493
FUBLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, USAPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REBERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION OF SEQ ID NOS: 47374
SEQ ID NO 9086
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                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: polypeptide
US-09-964-662-2
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78.0%; Score 46; DB 10; Length 200;
Best Local Similarity 90.9%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 1; Indels
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US-10-437-963-122700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                              TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 69.27
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                                                                                                                                                                                                                                                                                                              1 ALAAAKAAKYG 11
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US-10-369-493-9086
SEQ ID NO 2
LENGTH: 200
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                                                                                                FEATURE:
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Gaps

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Sequence 340008, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Cao, Youwai
APPLICANT: Cao, Youwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                      Score 38; DB 15; Length 129;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.4%; Score 38; DB 9; Length 149; 72.7%; Pred. No. 56;
                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31161C.1.pep
US-10-424-599-209451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PLILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209451
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 6936, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                    Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                               |:| :|||| | 61 AMAHLEAAKYGGA 73
                                                                                                                                                                                                                                                          1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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US-10-425-115-340008
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APPLICANT:
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APPLICANT:
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Publication No. US2004031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Kovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Applicant Soy Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
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          Gaps
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            Indels
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            1; Mismatches
                                                                                                                                                           Sequence 116, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
                                                                                                                                                                                                                                 Miao, Guo-Hua
Falco, Saverio Carl
                                                                                                                                                                                                                                                                                 Famodu, Omolayo O. Odell, Joan T.
                                                                                                                                                                                                                                                                                                                Meyers, Blake
Thorpe, Catherine
Weng, Zude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 ALSAAKEEKFGSA 176
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            Conservative
                                                                             391 ALAAANATRYG 401
                                             1 ALAAKKAAKYG 11
                                                                                                                                                                                                                                                                   Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-078-929-116
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Best Local Similarity
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US-10-424-599-209451
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Sereory J.
APPLICANT: Slater, Sereor C.
APPLICANT: Slater, Sereor C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPERSSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PELING DATE: 2003-02-28
PRIOR PELICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 463
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: MacBeth, Kyle J.
APPLICANT: Milliamson, Mark
TITLE OF INVENTION: 22012, A No. US20020156264Alel Human Carboxypeptidase
FILE REFRENCE: 5800-38
CURRENT APPLICATION NUMBER: US/09/345,469
PRIOR APPLICATION NUMBER: US/09/345,469
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                               64.4%; Score 38; DB 13; Length 233; 90.0%; Pred. No. 89;
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                                                                                                                                                                                                                       1; Indels
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    PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10068134
Publication No. US20020156264A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                 Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
US-10-369-493-9096
                                                                                                                                        US-10-056-744B-4
                                                                                  LENGTH: 233
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                                                                                                                                                                                 Query Match
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Pred. No. 60;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_62799C.1.pep
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Publication No. US20020193303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
TITLE OF INVENTION: HYDROLASE AND USES THEREFOR
FILE REPERENCE: MPI2001-026PIRNM
CURRENT APPLICATION UNMERR: US/10/056,744B
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/264,167
                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_73254C.1.pep
US-10-425-115-340008
                                                                                                                            ORGANIAN: Zea mays
FEATURE:
NAME/KEY: unsure
COCATION: (1)..(159)
OTHER INFORMATION: unsure at all Xaa locations
FILE REFERENCE: 38-21(5322)B
CURRBIY APPLICATION NUMBER: US/10/425,115
CURRBIY FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                             64.48;
76.98;
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61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              100 ALAAAAAAAAGAA 112
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      1 ALAAAKAAKYGAA 13
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Matches 8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-437-963-163840
                                                                          SEQ ID NO 340008
LENGTH: 159
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LENGTH: 177
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US-10-056-744B-4
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US-10-425-115-353761

i Sequence 353761, Application US/10425115

j Bublication No. US20040214272A1

j GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cor, Yongwei

TITLE OF INVENTION: Notleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Notleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Notleic Acid Molecules and Other Molecules Associated With

TITLE REPERENCE: 38-21 (52322)

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 353761

LENTH: 1.52

LENTH: 1.52
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Publication No. US20040214272A1
General Information:
APPLICANT: La Rosa Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Anou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Numbers: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                  Gaps
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Pred. No. 86;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 17; Length 152; . 86;
Score 37; DB 17; Length 86; pred. No. 48; 2; Indels 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Clone ID: MRT4577_85804C.1.pep US-10-425-115-353761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Clone ID: MRT4577_85810C.1.pep
US-10-425-115-353768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.7%; Score 37; DB 69.2%; Pred. No. 86; ative 0; Mismatches
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        62.7%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
        Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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12 IAASKTAQYGKA 23
                                                                                            2 LAAAKAAKYGAA 13
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Best Local Similarity
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Best Local Similarity
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ORGANISM: Zea mays
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US-10-425-115-353768
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Shou, Yinua
APPLICANT: Shou, Yinua
APPLICANT: Shou, Yinua
APPLICANT: Shou, Yinua
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 221398
LENGTH: 86
LENGTH: 86
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                                                                                                                                                                                Length 463;
                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                  Score 38; DB 14;
Pred. No. 1.8e+02;
0; Mismatches 2,
               TYPE: PRT
ORGANIEM: Chloroflexus aurantiacus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(463)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-9096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 221398, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8449, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Ralstonia metallidurans
                                                                                                                                                                                      64.48;
81.88;
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403 AVAAANATEYGLA 415
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Best Local Similarity 61.5°
Best Local 8; Conservative
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Best Local Similarity 81.0.
Local 9; Conservative
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ORGANISM: Zea mays
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US-10-425-115-221398
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US-10-369-493-8449
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TYPE: PRT
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                Sequence 368385, Application US/10425115
Sequence 368385, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 368385
LENGTH: 152
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Subblication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

FILE REPERENCE: 38-21(53377) BB

CURRENT APPLICATION NUMBER: US/10/739,930

SUBPRESS FILE OF DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 8468
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Pred. No. 86;
0; Mismatches 4; Indels
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US-10-739-930-8468
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; OTHER INFORMATION: Clone ID: MRT4577_99138C.1.pep
US-10-425-115-368385
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PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(152)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 69.2%;
Matches 9; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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ORGANISM: Zea mays
US-10-425-115-368385
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; Sequence 353760, Application US/10425115 ; Publication No. US20040214272A1

RESULT 30 US-10-425-115-353760

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GENERAL INFORMATION:

A PAPLICANT: La Rosa, Thomas J.
A PAPLICANT: La Rosa, Thomas J.
A PAPLICANT: A Rosalic, David K.
A PAPLICANT: Zhou, Yihua

A PAPLICANT: Zhou, Yihua

A PAPLICANT: Zhou, Yihua

A PAPLICANT: Zhou, Yihua

A PAPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing Secoing
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	protein search, using sw model	November 19, 2004, 15:19:20 ; Search time 2.65677 (without alignments) 1755.321 Million cell	US-09-743-818A-13 : 59 : ALAAAKAAKYGAA 13	e: BLOSUM62 Gapop 10.0 , Gapext 0.5	2002273 seqs, 358729299 residues	of hits satisfying chosen parameters: 2002273	eq length: 0 eq length: 200000000	.ng: Minimum Match 0% Maximum Match 100% Listing first 100 summarion	A_Geneseq_23Sep04:	1: geneseqp1980s.* 2: geneseqp190s.* 3: geneseqp200s:*			8: geneseqp2004g:*	. is the r eater than	ved by analysis of the total score distribut	SUMMARIES	Query Match Length DR ID		100.0 171 3 AAY69137	100.0 183 2 AAY01311 100.0 183 3 AAY69138	100.0 200 2 AAY01305 100.0 216 2 AAY01310	100.0 472 4 AAB88422	100.0 663 7 ADM03792	100.0 698 2 AAY01302	100.0 698 3 AAY69069 100.0 712 3 AAB08630	100.0 730 2 AAW46315 100.0 730 3 AAB08631	100.0 730 5 AAO17360	100.0 730 8 ADQ19747 100.0 731 3 AAY69068	100.0 731 4 AAB66557 100.0 731 6 ABH08725	100.0 731 7 ADL96420 100.0 733 2 AARS6653	9 100.0 733 2 AAY01301 AAY01301 9 100.0 757 7 ABG75223	100.0 757 7 ADP65160
	OM protein -	Run on:	Title: Perfect score Sequence:	Scoring table	Searched:	H	Minimum DB seq Maximum DB seq	Post-processing:	Database :					Pred. No score gr	and is		Result Score						o	, с	N 63	4 4 ∩ 0	9 (~ oo (on (c)	7 7	23 59 24 59	70

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Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                             New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                          Amino acid sequence of a human tropoelastin derivative
                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 133-134; 136pp; English.
                                                                                                                                                                                                       98AU-00004723
                      (first entry)
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                                                                                                                                     WO200004043-A1.
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                                                                                                                                                                                                       17-JUL-1998;
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                      30-MAY-2000
                                                                                                                                                                                                                                                                                                              cell growth
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 AAY69137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells contraining vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELGamma excluding the product encoded by exon
                                                                                                                                                                                               Tropoelastin; hTB; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
  Adf05791 Bacterial
Ada33347 Acinetoba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
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                                                   ALIGNMENTS
                                                                                                                                                                             Human tropoelastin derivative SHELgamma
    ADF05791
ADA33347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69137 standard; protein; 171 AA.
                                                                                                           AAY01304 standard; protein; 147 AA
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nes 13; Conserv
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                                                                                                                                                                                                                                                             Synthetic.
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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudere. The tropoelastin derivatives provide contact with serum or polypeptides containing tropoelastin derivative derivatives, and other polypeptides containing tropoelastin derivative derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents of from inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothalial cells, fibrollasts, osteocytes, chondrootres and patelete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptidomimetics that mimic the protease cleavage site in tropelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 3; Length 171; 100.0%; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY01311 standard; protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycoseminoglycan (6AG))-binding properties. Cells contending vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or Apbrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, epproducts. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELZ6-36 excluding exon 26A product
Tropoelastin, hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                 New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 59; DB 2; Length 183; 100.0%; Pred. No. 0.022; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a human tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69138 standard; protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 39; Page 11; 82pp; English
                                                                                                                                                                                    98WO-AU000564.
                                                                                                                                                                                                                   97AU-00008117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-AU000580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98AU-00004723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 ALAAKAAKYGAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
ses 13; Conservative
                                                                                                                                                                                                                                                                                                                    WPI; 1999-132162/11.
                                                                                                                                                                                                                                                  (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200004043-A1
                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                               WO9903886-A1
                                                                                                                                                                                                                   18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1998;
                                                                                                                                                                                   17-JUL-1998;
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                                                                                                                                                  28-JAN-1999
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                                                                                    Synthetic
                                                                                                                                                                                                                                                                                   Weiss AS;
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                                                                    Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative activity in the tropoelastin derivatives and other polypeptides containing tropoelastin derivative. Cerivatives, and other polypeptides containing tropoelastin derivative activity of erived protease-susceptibility sites, are useful in human or veterinary candior, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, spithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that minic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and are used for containing and ar
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                                                                                                                                                                      New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tropoelastin, hTE; elastin, glycosaminoglycan, GAG-binding, medical, pharmaceutical; veterinary, cosmetic application, anti-wrinkle, food, hand lotion, surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 3; Length 183; 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                            Disclosure; Page 134-135; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tropoelastin derivative SHELgamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY01305 standard; protein; 200 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 ALAAAKAAKYGAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
hes 13; Conservative
                    (UNSY ) UNIV SYDNEY
                                                                                                                  WPI; 2000-182399/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 183 AA;
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                                                                                                                                                                                             cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999.
                                                                      Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY01305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AAB88422;
                                                                                                                                                                                                                                  RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically algrosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives
                                                                                                                               comprising the nucleic acids encoding the variants overlap comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELGamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                tropoelastin
                                                                                              The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                    New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
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                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 2; Length 200; 100.0%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tropoelastin derivative SHEL26-36.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01310 standard; protein; 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 35; Page 11; 82pp; English
                                                                           Claim 15; Fig 8; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-AU000564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97AU-00008117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                 1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                       62 ALAAAKAAKYGAA 74
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-132162/11.
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  MPI; 1999-132162/11
                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                           AA;
               N-PSDB; AAX27707
                                                                                                                                                                                                                                                           Sequence 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9903886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998;
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                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY01310;
                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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This invention relates to nucleic acid sequences AAF93744 - AAF93916

which encode human secretory or membrane proteins represented by AAB88317

- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and

AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the

invention. The invention also includes methods for the production of

antibodies directed against the proteins, and CDNA sequences, which can

be used in vaccines. The polynucleotide sequences can be used in gene

therapy. The polynucleotide sequences and the proteins they encode may be

used in the prevention, treatment and diagnosis of diseases associated

with inappropriate secretory protein/membrane protein expression. The

nucleic acids and complementary sequences may also be used as DNA probes

con diagnostic assays (e.g. polymerase chain reactions (FCR)) to detect

and quantitate the presence of similar nucleic acid sequences in samples.

They may also be used to study the expression and function of secretory

They may also be used as antigens in the production of antibodies

polypeptides may be used as antigens in the production of antibodies

against them and in assays to identify modulators (agonists and
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or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiwrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHEL26-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretory proteins/membrane proteins, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy or as candidate target molecules in drug development
                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                               Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                     Score 59; DB 2; Lengua --
Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human membrane or secretory protein clone PSEC0191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB88422 standard; protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥ ;
                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000EP-00114090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 ALAAKAAKYGAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                    Sequence 216 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 13;
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antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes

Sequence 472 AA;

Gaps ; 0 4; Length 472; 0; Indels 100.0%; Score 59; DB 4; 100.0%; Pred. No. 0.06; iive 0; Mismatches Conservative Best Local Similarity 13; Query Match Matches

à

ADB64761 standard; protein; 617 AA. ADB64761 RESULT

ADB64761;

Human protein encoded by clone NT2RP70003110.

(first entry)

04-DEC-2003

Human, pharmaceutical, diagnostic, gene therapy; tissue regeneration; cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein; osteoporosis, neurological disease; cancer; tumour.

Homo sapiens.

EP1308459-A2. 07-MAY-2003. 28-MAR-2002; 2002EP-00007401.

05-NOV-2001; 2001JP-00379298

25-JAN-2002; 2002US-00350978

(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y; Sugiyama T, J, Isono Y, Yoshikawa T, Yamamoto J, Isogai T, Seki N,

WPI; 2003-450961/43. N-PSDB; ADB62791. New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy

Claim 1; Page; 222pp; English.

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide decide for detecting the polynucleotide and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or

of gene therapy. The genes are involved in tissue and/or of the regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteopornosis, the univological diseases. Cancer, thmours. The CDNA may be used to regulate sequence presented is a protein of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the specification, but is based on sequence information supplied by the European Patent Office. or as targets for regulation of their expression and activity, 88888888888888888888

Sequence 617 AA;

0

Gaps o O 100.0%; Score 59; DB 7; Length 617; 100.0%; Pred. No. 0.08; 0; Indels 0; Mismatches 13; Conservative Query Match Best Local Similarity Matches

6

497 ALAAAKAAKYGAA 509 1 ALAAAKAAKYGAA 13 ð Dp

ADM03792 RESULT

ADM03792 standard; protein; 663 AA.

ADM03792;

20-MAY-2004 (first entry)

Human protein of the invention SEQ ID NO:2477

human; gene therapy; diagnostic marker; pharmaceutical.

Homo sapiens.

EP1347046-A1

24-SEP-2003.

12-APR-2002; 2002EP-00008400. 22-MAR-2002; 2002JP-00137785.

(REAS-) RES ASSOC BIOTECHNOLOGY.

Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y; ., Sugiyama T, J, Isono Y, I Yamamoto J, Isogai T, Seki N,

WPI; 2003-723558/69,

N-PSDB; ADM01349.

New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

Claim 1; SEQ ID NO 2477; 305pp; English.

The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM01316 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM01759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.

Sequence 663 AA;

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N-PSDB; ADE40133
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY01302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                        NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; artherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheiner's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Gasman SJ;
Voss BZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
                                        Gaps
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0
   100.0%; Score 59; DB 7; Length 663; 100.0%; Pred. No. 0.086; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  ADE40134 standard; protein; 692 AA.
                                                                                                                                                                                                                                                                                                                           Human NOV16b protein - SEQ ID 40.
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2001US-0311292P.
2001US-0313201P.
2001US-0313201P.
2001US-0313702P.
2001US-0313702P.
2001US-0313702P.
2001US-0314031P.
2001US-0314031P.
2001US-0315403P.
2001US-0315403P.
2001US-0315403P.
2001US-03234P.
2001US-034033P.
2001US-034033P.
2001US-034033P.
2001US-034033P.
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2002US-0373989P.
2002US-0374632P.
2002US-0386971P.
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2001US-0310951P.
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                                                                                                                    525 ALAAKAAKYGAA 537
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                                                                                 1 ALAAAKAAKYGAA 13
                                            Conservative
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           Query Match
Best Local Similarity
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13-AUG-2001;
16-AUG-2001;
17-AUG-2001;
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28-AUG-2001;
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17-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, encorportective, nootropic, antidiabetic, immunosuppressive, anti-HIV, gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertenaton, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                   of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors
New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                   The invention relates to a novel NOVX polypeptide. The polypeptide invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
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                                                                                                                                                                                                         Claim 1; SEQ ID NO 40; 560pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01302 standard; protein; 698 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                               pharmacogenomics.
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endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoclastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

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inhibition, particularly of smooth muscle

Length 698;

Score 59; DB 3; Pred. No. 0.091;

100.0%;

Local Similarity

Matches

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Gaps

; 0

Query Match

Sequence 698 AA;

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used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable ddG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the synthetic human tropoelastin variant SHELGelta26A
                                                                                                                                                                                                                                                                                                                                                                              Tropoelastin, derivative, SHEL-delta-26a, SHEL, proteolysis, protease, antiwrinkle, hand lotion, bulking agent, chemotaxis, proliferation, growth inhibition, peptidomimetic, lung damage, elastin, cancer, metastasis; blood clotting.
comprising the nucleic acids encoding the variants or derivatives are
                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human reduced tropoelastin derivative.
                                                                                                                                               100.0%; Score 59; DB 2; Length 698; 100.0%; Pred. No. 0.091;
                                                                                                                                                                          0; Indels
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                AAY69069 standard; protein; 698 AA.
                                                                                                                                                                        .,
                                                                                                                                                                                                                    560 ALAAKKAAKYGAA 572
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                              1 ALAAAKAAKYGAA 13
                                                                                                                                                                        Conservative
                                                                                                                                                           Local Similarity
                                                                                                                       Sequence 698 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                               30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                       AAY69069;
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                   AAY69069
88888888888888
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WO200050068-A2
Homo sapiens.
                                                                                                                                                                                                                                                                                                         26-FEB-1999;
                                                                                                                                                    31-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is conceased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in competitive inhibition of protease activity. The tropoelastin derivatives provide derivatives, and other polypeptides containing tropoelastin derivative-convertived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 110-112; 136pp; English.
                                                                                                                                                                                                                                                                                99WO-AU000580.
                                                                                                                                                                                                                                                                                                                                                         98AU-00004723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-182399/16.
                                                                                                                                                                                                                                                                                                                                                                                                                             (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ61144.
                                                                                                            WO200004043-A1.
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19-JUL-1999; 17-JUL-1998;

cell growth.

Weiss AS;

27-JAN-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastin are used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities etimulating: inhibiting the proliferation of smooth muscle cells in vivo; and regulating the migration of smooth muscle cell in vivo; and may be used for the prophylaxis or treatment of a disorder characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by diminished capacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                              Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell function; atheroscierosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human elastin. Peptides derived from
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
       0;
   0; Indels
                                                                                                                                                                                                                                                           Amino acid sequence of a human elastin polypeptide.
   Mismatches
                                                                                                                                                        AAB08630 standard; peptide; 712 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 46; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00258217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UTAH ) UNIV UTAH RES FOUND.
                                                            560 ALAAAKAAKYGAA 572
                                                                                                                                                                                                                               (first entry)
                                 1 ALAAAKAAKYGAA 13
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-533134/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 712 AA;
                                                                                                                                                                                                                              20-DEC-2000
                                                                                                                                                                                           AAB08630;
                                                                                                                     RESULT 13
                                                                                                                                       AAB08630
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Gaps

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100.0%; Score 59; DB 2; Length 730; 100.0%; Pred. No. 0.095; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity

Matches

Sequence 730 AA;

X 8

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                                                                                                                                                                                                                                                                                                                                                                            New non-natural polypeptide with multiple beta-sheet, beta-turn
structures - particularly based on human elastin, useful for coating
prostheses, as wound dressings, etc., allows ingrowth of cells.
                 Gaps
                                                                                                                                                            MFU-1; minimal functional unit; elastin; human; fibrous protein; beta-sheet; coating; wound dressing.
                                                                                                                                           Human elastin containing non-natural polypeptide MFU-1 sequence.
                 .,
Length 712;
                 0; Indels
Score 59; DB 3;
Pred. No. 0.093;
Mismatches 0
                                                                                                                                                                                                                   374. .499
/note= "MFU-1 polypeptide"
                                                                                                                                                                                                                                                                                                                                              Rothstein SJ;
                                                                                                                                                                                                                                                                                                                             (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                         Location/Qualifiers
                                                                                            AAW46315 standard; protein; 730 AA.
                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 1B; 39pp; English.
                  0;
  100.0%;
                                                                                                                                                                                                                                                                                                     97US-00911364.
                                                                                                                                                                                                                                                                            97WO-CA000560
                                                                                                                                                                                                                                                                                             96US-0023552P
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                Keeley FW,
                                  1 ALAAAKAAKYGAA 13
                  Conservative
                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-145551/13.
  Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                Rothstein A,
                                                                                                                                                                                                                                                                             07-AUG-1997;
                                                                                                                                                                                                                                                                                             07-AUG-1996;
                                                                                                                                                                                                                                            WO9805685-A2
                                                                                                                                                                                                                                                                                                     07-AUG-1997;
                                                                                                                                                                                           Homo sapiens
                                                                                                                                23-JUL-1998
                                                                                                                                                                                                                                                             12-FEB-1998
                   13;
                                                                                                               AAW46315;
                                                                                                                                                                                                                   Protein
                     Matches
                                                                              RESULT 14
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Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation; smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.

Fusion protein comprising human elastin and c-myc.

(first entry)

20-DEC-2000

AAB08631;

AAB08631 standard; peptide; 730 AA.

RESULT 15

AAB08631

593 ALAAKAAKYGAA 605

a a à

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1 ALAAAKAAKYGAA 13 13; Conservative

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Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
This represents the human elastin sequence containing the minimal curcional unit (MTU)-1 polypeptide of the invention. This MFU-1 is a functional unit (MTU)-1 polypeptide of the invention. This MFU-1 is a functional unit (MTU)-1 polypeptide of the invention. This MFU-1 is a cont a naturally occurring fibrous protein. Each beta-sheet structure has cont a naturally occurring fibrous protein. Each beta-sheet structure has considered that can take part in crosslinking. The polypeptide at an anino acid that can take part in crosslinking. The polypeptide consolidate in the MFU polypeptides are self-aligning peptides. Spider silk protein. The MFU polypeptides are self-aligning peptides can easing the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or compared to coat prostheses made of animal or synthetic material or control particularly for use as blood vessel or heart valve replacements. Or high-tensile streagh materials, e.g. ropes or parachute cord.

Cor high-tensile streagh materials, e.g. ropes or parachute cord.

Cor high-tensile streagh materials and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic control parameterials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider silk protein
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The present sequence represents a fusion protein, comprising human clastin and c-myc, preceded by a His tag. The protein is used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell compositions comprise at least one elastic fibre, elastins, tropoelastins compositions comprise at least one elastic fibre, elastins, tropoelastins contributing the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cells in vivo; stimulating the prophylaxis or treatment of adisorder characterized by contributed capacity to regulate smooth muscle cell function such as diminished capacity to regulate smooth muscle cell function such as atherical prophylaxis or treatment of adisorder characterized by a characterized by a characterized by an elastic streams and/or dissection. Disorders which may be treated atherically and an elastic fiscentian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 3; Length 73
100.0%; Pred. No. 0.095;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 48; 79pp; English.
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Elastin based compositions useful for treating atherosclerosis,

WPI; 2000-533134/48.

Keating MT, Li DY;

99US-00258217.

26-FEB-1999;

(UTAH) UNIV UTAH RES FOUND

28-FEB-2000; 2000WO-US002526.

WO200050068-A2.

31-AUG-2000

Unidentified Homo sapiens

Synthetic.

1 ALAAAKAAKYGAA

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The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a control sample. A reduced level is indicative of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, algebyde debydrogenase 6, gravin, phospholipase C epsilon, elastin, insulin-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet derived growth factor receptor alpha, laminin M chain, subtilisin like protein PACE4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human elastin
                                                                                                                                                                                                                                               Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 59; DB 5; Length 730; 100.0%; Pred. No. 0.095; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Regidor P, Scotti \mathbf{S}_i
                                                                                            AA017360 standard; protein; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 15-16; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2001; 2001EP-00250300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000; 2000DE-01048633
601 ALAAKAAKYGAA 613
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-317413/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCHD ) SCHERING AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 730 AA;
                                                                                                                                                                                                             Human elastin
                                                                                                                                                                                                                                                                                                                                                                                                                         EP1191107-A2
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                        19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2002
                                                                                                                                  AA017360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.
                                                                           AA017360
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Winterhager E;

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both samples, where a higher level protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-uprequlated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                       soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;0
                                                                                    tissue sarcoma-upregulated protein - SEQ ID 2566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 8; Length 730; 100.0%; Pred. No. 0.095; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a human tropoelastin splice form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 2566; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69068 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                         Zlotnik A;
                                                                                                                                                                                                                                                                                                                                    (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                   26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                26-NOV-2003; 2003WO-US038193
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 ALAAAKAAKYGAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALAAAKAAKYGAA 13
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                       Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-441208/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 730 AA;
                                                                                                                                                                                           WO2004048938-A2
                                                                                                                                                          Homo sapiens.
                                                 26-AUG-2004
                                                                                                                                                                                                                              10-JUN-2004.
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                                                                                      Human soft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                       Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
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Gaps

0;

ADQ19747 standard; protein; 730 AA.

RESULT 17 ADQ19747 ID AD01

592 ALAAAKAAKYGAA 604

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Human; elastin; minimal functioning unit; MFU; beta-sheet/beta-turn structure; fibrous protein; prosthesis; blood vessel replacement; heart replacement valve; burn; wound; lamprin; spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor; platelet activation inhibitor; non-thrombogenic; cell infiltration; non-immunogenic; blocompatible; high tensile strength; elasticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a minimal functional unit (MFU) of human elastin polypeptide. This protein is useful in a cosmetic material or a prosthetic material such as prosthesis for blood vessel replacements, for heart valve replacement, tissue replacement, for covering burns, for covering wounds and stents
                                                                                                                                                                                                                                                                                                    Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide useful in prosthesis, has a secondary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 4; Length 731; 100.0%; Pred. No. 0.096; ... Mismatches 0; Indels
                                                                                                                                                                                                          Stahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                               Rothstein S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothstein S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU08725 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HSCR-) HSC RES & DEV LP.
(PROT-) PROTEIN SPECIALTIES LTD.
                                                                                                                                    (PROT-) PROTEIN SPECIALTIES LTD. (HSCR-) HSC RES & DEV LP.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human elastin mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00340736.
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                                       29-JUN-2000; 2000WO-US017829.
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Query Match

Best Local Similarity luv...

Best Local 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 ALAAAKAAKYGAA 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALAAAKAAKYGAA 13
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                                                                                                                                                                                                               Rothstein A, Keeley F,
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                                                                                                                                                                                                                                                            WPI; 2001-102886/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 731 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-1996;
07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6489446-B1
                                                                                         29-JUN-1999;
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04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasticity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU08725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence considered so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatived proteas-susceptibility sites, are useful cropoelastin derivatived proteas-susceptibility sites, are useful cin human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand or susful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or competition, for inhibiting or controlling localized growth of cancers or competitions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 0.096;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimal function unit; MFU; human; elastin prosthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human elastin protein without signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 107-109; 136pp; English
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB66657 standard; protein; 731 AA.
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503. .504
515. .516
564. .565
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Matches 13; Conserv
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                      Cleavage-site
Cleavage-site
Cleavage-site
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                                                                                                 Cleavage-site
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                                                                                                                                                                                                                                                                                            17-JUL-1998;
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                                                                                                                                                                                             27-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell growth
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                                                                                                                                                                                                                                                                                                                                                                                           Weiss AS;
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Gaps

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the invention describes a polypeptide (1) comprising a minimal functioning unit (MFU) which is present in the sequence of human elastin and comprised of at least three beta-sheet/beta-turn structures, and at least cone amino acid residue that participates in cross-linking, and not a naturally occurring fibrous protein. The MFU material can be used to construct human elastin-like prostheses such as tubes for blood vessel burns or wounds to promote healing MFUs can be co-aggregated with other proteins, for e.g. collagen, to provide prosthesis material that resembles the natural structural materials of the body. MFUs modeled on lamprin and other fibrous proteins of different applications, for e.g. or ords and ropes for use in parachutes and in cosmetics. Coating synthetic prosthesis with MFUs modeled on human elastin significantly in thibits platelet binding and activation. The human-like MFU material is complibits platelet binding and activation. The human-like MFU material is considerably smaller than the composition. The MFU is considerably smaller than the composition and compliance or express in quantity, to handle in solution and to manipulate for express in thrombogenic and provides a friendly environment for cell infiltration. Enrompagenic and provides a friendly environment for cell infiltration. Enrompagenic, thus providing a truly biocompatible material. MFUs modeled on lamprin and other fibrous proteins errearies and be arriefly of material materials and providing a truly biocompatible material. MFUs materials when the environment and materials of materials errearies and materials of materials errearies and have a directly environment of main and any arriety of materials errearies and be arriefly environment. Menus providing a truly biocompatible material materials of materials errearies en beside or all materials errearies errearies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human elastin on which the MFU peptides of the invention are based
                ď
   three beta-sheet/beta-turn structures, and is not
                                                                                                                                                                       comprising a minimal
                                                                                                                                                             invention describes a polypeptide (I)
                                 naturally occurring fibrous protein.
                                                                                                 Claim 1; Fig 1B; 21pp; English.
      characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 731 AA;
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; Query Match
100.0%; Score 59; DB 6; Length 731;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 13; Conservative 0; Mismatches 0; Indels

0;

Gaps

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ADL96420 standard; protein; 731 AA. 20-MAY-2004 ADL96420; RESULT 21 ADL96420

Human elastin protein fragment. (first entry)

fibrous protein; prosthesis; elastin; lamprin; spider silk protein; blood vessel; wound; burn healing; collagen.

Homo sapiens

location/Qualifiers .160 Region Region

'note= "region specifically claimed in claim /note= "region specifically claimed in claim 374. .499 .367 Region

.9 .9 .9

9

/note= "region specifically claimed in claim 607. .717 /note= "region specifically claimed in claim

US2003166846-A1

Region

04-SEP-2003.

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This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous shottly. The invention also describes a prosthesis comprising an animal, metal or synthetic material, where the surface is coated with the polypeptide, a cosmetic material, where the surface is coated with the polypeptide, a material comprising the polypeptide, a material comprising the polypeptide or a high tensile strength material comprising the polypeptide consisting essentially of a material comprising the polypeptide consisting essentially of a portion of the polypeptide consisting essentially of a portion of the mind and a lastin comprising at least three beta sheet/beta turns, conspiring at least three beta sheets/beta turns, and (d) a sheets/beta turns, (c) a polypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, a polypeptide having the primary comprising at least three beta sheets/beta turns, a polypeptide having the primary a scondary structure of a naturally of a spider silk protein and a scondary structure of a naturally of a spider silk protein and secondary structure of a portion of a naturally of a portion of a naturally of spider silk protein and secondary structure of aportion of a naturally of spider silk protein and secondary structure of an animal luni (MPU) of the invention is construct human elastin-like prostheses such as tubes for blood the spider silk protein of construct human elastin-like prostheses such as tubes for blood of the sample collagen, to provide prostheses such as wound or burn channel structural materials of the body. The MPU based material is subject to infiltration of cells growing in the parental that resembles the containing materials proposed for prostheses.

"Xx xx xx and do the prostheses are permanent living containing materials proposed for prostheses."
                                                                                                                                                                                                                                                                                                                                                            Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns.
                                                                                                                                                                                                                                                                     Rothstein S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 1B; 17pp; English.
                        28-SEP-2001; 2001US-00964662.
                                                                          96US-0023522P.
                                                                                                                       99US-00340736
                                                                                                                                                                                                                                                                Rothstein A, Keeley F,
                                                                                                                                                                  ROTHSTEIN A.
                                                                                                                                                                                          KEELEY F.
ROTHSTEIN S.
                                                                                                                                                                                                                                                                                                                WPI; 2003-898105/82.
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                                                                     07-AUG-1996;
                                                                                              07-AUG-1997;
29-JUN-1999;
                                                                                                                                                                    (ROTH/)
                                                                                                                                                                                                                 (ROTH/)
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Gaps . 0 100.0%; Score 59; DB 7; Length 731; 100.0%; Pred. No. 0.096; tive 0; Mismatches 0; Indels 13; Conservative Local Similarity Query Match Matches

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ò g RESULT 22 **AAR**56653 AAR56653;

AARS6653 standard; protein; 733 AA.

(first entry) (revised) 25-MAR-2003 22-MAR-1995 XEXHEXEX

Synthetic human tropoelastin (SHEL).

Synthetic.

Weiss AS,

variants.

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The present invention relates to the use of an agent that promotes elastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin polymerisation, increasing F:G actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis, or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells is useful for decreasing or preventing occlusion of a body
                                                                                          The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are useful to produce the proteins recombinantly. The tropoelastin derivatives have to produce the proteins recombinantly. The tropoelastin derivatives have the proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable &AG-binding properties, products. The hybrid protein have controllable &AG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59; DB 2; Length 733; 100.0%; Pred. No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page 138-141; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG75223 standard; protein; 757 AA.
                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tropoelastin protein.
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Best Local Similarity 100.
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                                                                  Disclosure, Fig 1; 82pp;
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 733 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human synthetic tropoelastin is susceptible to hydrolytic breakdown of the crosslinks. Such material may be useful in e.g. surgical applications, where the gradual loss of material over time is intended. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic polynucleotide(s) - encode recombinant tropoelastins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 59; DB 2; Length 733; 100.0%; Pred. No. 0.096; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of synthetic human tropoelastin SHEL.
           Tropoelastin; pharmaceutical; surgical dressing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY01301 standard; protein; 733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 30; 77pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                   Martin SL;
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                                                                                                                                                                                                                                                                                           (UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-263633/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ70941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-1997;
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                                                                                                                                                                                                                           22-DEC-1992;
28-JUN-1993;
                                                                                                                                                                                     16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1999
                                                                                                   WO9414958-A1
                                                                                                                                           07-JUL-1994
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Synthetic

AAY01301

RESULT 23
AAY01301
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Gaps

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                actin stress fiber formation or actin polymerization, increasing F:g actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis following angloplasty), or preventing stenosis. It is also useful in manufacturing a medicament for the treatment or prevention of occlusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunosmodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
            promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of further comprises: a treatment of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                Gaps
  vessel by smooth muscle cells, decreasing vascular obstruction,
                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                   100.0%; Score 59; DB 7; Length 757; 100.0%; Pred. No. 0.099; o. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP65160 standard; protein; 757 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002; 2002WO-US035433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2001; 2001US-0336220P
                                                                                                                                                                                                                                                                                                                                   619 ALAAKKAKYGAA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                              1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thorton SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-712740/67.
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENBANK, NP 000492
                                                                                                                                                                            Sequence 757 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ımmune; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                         invention
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Best Local S
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efficacy of a candidate drug in vitro for the treatment of collagen-
induced arthritis; and reducing the symptoms associated with collagen-
induced arthritis: The compositions of the invention have the following
activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
antigout, antinflammatory, dermatological, and immunomodulatory. The
methods and compositions of the present invention are useful for
methods and compositions of the present invention are useful for
theumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
immune disease caused by an infectious agent. This sequence represents a
protein sequence relating to the genes used in the analysis and treatment
of autoimmune diseases or arthritides. Note: This sequence is not shown
in the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabelic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antischmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabeters; AIDS; multiple sclerosis; graft-versus-host disease; AIDA; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 59; DB 7; Length 757; 100.0%; Pred. No. 0.099; ive 0; Mismatches 0; Indels
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2001US-0313201P.
2001US-0313415P.
2001US-0313643P.
2001US-0313702P.
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2001US-0310544P.
2001US-0310951P.
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2001US-0311979P.
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2002US-0354591P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALAAAKAAKYGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue typing; human; NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 757 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003064589-A2.
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16-AUG-2001;
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17-AUG-2001;
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28-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Sequence 12 AA;
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17-JUL-1998;
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                                                                                                                                                           cell growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                       Weiss AS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and synaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosals, hypertension, cancer, obesity, diabetes, Alba, multiple solerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as butilised to probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                              Anderson DW;
                                                                                                                                       Kekuda R. Miller CE, Patturajan M, Pena CEA, Rieger DK; Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ; Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson I Guo X, Zhong M Gerlach VL, Hjalt T, Rastelli L, Spytek KA; Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ; Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidomimetic of a cleavage site of a human tropoelastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Pred. No. 0.31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 38; 560pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY69144 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%;
     19-APR-2002; 2002US-0373825P.
19-APR-2002; 2002US-0373989P.
23-APR-2002; 2002US-0374632P.
07-UNN-2002; 2002US-0386971P.
01-AUG-2002; 2002US-00210172.
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591 ALAAARAAKYGAA 603
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                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                        WPI; 2003-663472/62.
N-PSDB; ADE40131.
                                                                                                                                                                                                                                                                                                                                                                                                   pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 711 AA;
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                                                                                                                                                                                                                                         Alsobrook J
Smithson G;
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AAY69144;

RESULT 27 AAY69144

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Query Match Best Loca Matches

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The present sequence represents a peptidomimetic of a cleavage site of a human tropoelastin. The specification describes human tropoelastin derivatives, in which a subsequence has been mutated so that cascaptability to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatived protease.

CC containing tropoelastin derivatives provide competitive proteining tropoelastin derivatived protease.

CC consection (e.g. antiwrinkle or hand locions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth commettics that mimic the protease cleavage site in tropoelastin epptidomimetics that mimic the protease cleavage site in tropoelastin contecting against lung damage caused by elastin, for inhibiting or containing localized growth of cancers or metastases, or to limit containing localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                   New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.0065; 
0; Mismatches 0; Indels
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100.0%; Pred. No. c...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        Claim 76; Page 73; 136pp; English.
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98AU-00004723.
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                                                                             (UNSY ) UNIV SYDNEY
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WPI; 1999-132162/11
   N-PSDB; AAX27705
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The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (6AG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical. pharmaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTB. The present sequence represents a human tropoelastin derivative SHEELdeltamodified New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants. Claim 7; Fig 3; 82pp; English. Sequence 660 AA;

Gaps ; Length 660; 0; Indels 93.2%; Score 55; DB 2; 100.0%; Pred. No. 0.43; 100.0%; Prec. ... Query Match
Best Local Similarity 100.v.

RESULT 29 AAY69135

30-MAY-2000 (first entry) AAY69135;

AAY69135 standard; protein; 515 AA.

Amino acid sequence of a human tropoelastin derivative.

Tropoelastin, derivative, proteolysis; protease, antiwrinkle, hand lotion; bulking agent; chemotaxis, proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

Homo sapiens.

WO200004043-A1.

27-JAN-2000.

99WO-AU000580. 19-JUL-1999;

98AU-00004723. 17-JUL-1998;

(UNSY) UNIV SYDNEY

Weiss AS;

WPI; 2000-182399/16

New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth

Disclosure; Page 131-133; 136pp; English.

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is

increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives competitive inhibition of protease activity. The tropoelastin derivative. Competitive inhibition of protease activity. The tropoelastin derivative competics (e.g. antiwarinkle or hand lotions), as bulking agents medicine, cosmetics (e.g. antiwarinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Competitive inhibitors of the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting %

Sequence 515 AA;

Gaps ·. 91.5%; Score 54; DB 3; Length 515; 92.3%; Pred. No. 0.49; Live 0; Mismatches 1; Indels Local Similarity 92.3 Query Match Best Loca Matches

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RESULT 30

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AAY69071 standard; protein; 571 AA. AAY6907

AAY69071;

(first entry) 30-MAY-2000

Amino acid sequence of a human tropoelastin derivative.

Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

Homo sapiens.

WO200004043-A1.

27-JAN-2000.

99WO-AU000580. 19-JUL-1999;

98AU-00004723. 17-JUL-1998;

(UNSY) UNIV SYDNEY

Weiss AS;

WPI; 2000-182399/16.

New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth

Disclosure; Page 115-117; 136pp; English.

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the so plats the derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be contact with serum or wound exudete. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative-derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary

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cc and for inducing chemotraxis. They are also useful for proliferation or cc and for inducing chemotraxis. They are also useful for proliferation or cc growth inhibition, particularly of smooth muscle cells, epithelial or cendothelial cels, fibroblasts, oshcorytes and platelets. Cc endothelial cels, fibroblasts, oshcorytes and platelets. Cc endothelial cels, fibroblasts, oshcorytes and platelets. Cc controlling localized growth of cancers of the protease, and are used for controlling localized growth of cancers or metastasses, or to limit C protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastasses, or to limit XX SQ Sequence 571 AA;

Query Match

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ALAMAKARAKYGAA 293

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Ade40132 Human ela
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Aay69158 Amino aci
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N-PSDB; AAZ61144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically dylvosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are useful to produce the proteins recombinantly. The tropoelastin derivatives pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the synthetic human tropoelastin variant SHELGelta26A
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pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
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macromolecular binding properties, useful e.g. as surgical implants.
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Aaw53520 A
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    AAW26344
AAW53520
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Best Local Similarity
Matches 698; Conserv
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Disclosure; Page 110-112; 136pp; English

The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is subsequence has been mutated so that susceptibility, to proteolysis is increased. The derivatives have with reduced susceptibility, and can be context with serum or wound exidate. The tropoelastin derivatives provide context with serum or wound exidate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative of derivatives, and other polypeptides containing tropoelastin derivative. Competitive inhibition, particularly sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents of growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, ottocase cleavage site in tropoelastin cendothelial cells, fibroblasts, ottocase cleavage site in tropoelastin protecting against lung damage caused by elastin, for inhibiting or protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

Sequence 698 AA;

Gaps 0; Length 698; Indels ; 0 DB 3; ; Score 3615; DB 3; ; Pred. No. 6.8e-202 0; Mismatches 0; 100.0%; 100.0%; Query Match
Best Local Similarity 100.
Matches 698; Conservative

09 9 GGVPGAIPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT GGVPGAIPGGVPGGVFYPGAGLGALGGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT

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RESULT 3

AA017360 standard; protein; 730

AA017360;

(first entry) 19-JUL-2002

Human elastin.

Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.

Homo sapiens

27-MAR-2002.

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21-AUG-2001; 2001EP-00250300.

25-SEP-2000; 2000DE-01048633

(SCHD) SCHERING AG.

Winterhager E; Kreft B, Kraetzschmar J, Haendler B, Scotti S; Hess-Stumpp H, Regidor P,

WPI; 2002-317413/36.

In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin

Claim 1; Page 15-16; 21pp; German.

The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a control sample. A reduced level is indicative of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, albebyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin, insulin-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet derived growth factor receptor alpha, laminin M chain, subtilisin like protein PACE4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human elastin

Sequence 730 AA;

Gaps 9 Length 730; 0; Indels Score 3602; DB 5; Pred. No. 4e-201; Mismatches 0; 99.6%; Conservative Query Match Best Local Similarity Matches 698;

9 98 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT

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120 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL

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            PGVYPGGVLPGARFPGVGVLPGPVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
                                                                      PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKF
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PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGI PGVGPFGGPQPFLGY
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                           Score 3602; DB 8;
Pred. No. 4e-201;
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                          Example 2; SEQ ID NO 2566; 210pp; English
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Best Local Similarity 99.1'
Marches 698; Conservative
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Tropoelastin, derivative, proteolysis; protease; antiwrinkle, hand lotion, bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                              New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                    Amino acid sequence of a human tropoelastin splice form.
                                                                                                                                                                                                                                                                                                    Disclosure; Page 107-109; 136pp; English
                                                                                                                 Location/Qualifiers
       AAY69068 standard; protein; 731
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AAY69068
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specification describes troposelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is reduced or proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease cropoelastin derivatived prived protease and other polypeptides containing tropoelastin derivatived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinke or hand or so bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth consecut for proliferation or growth inhibition, particularly of smooth consecut in tropoelastin derivatives are competitive inhibitors of characters and platelets. Peptidomimetics that mimic the protease consecution or growth inhibiting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or consecuting for inhibiting or controlling localized growth of cancers or consecuting passes beload clotting controlling localized growth of cancers or consecuting asses, or to limit protease activity that causes blood clotting
present sequence represents a human tropoelastin splice form. The
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Homo sapiens.
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                                                                                                                                                                                                                             DB 3; Length 731;
                                                                                                                                                                                                                         Score 3588,5; DB 3
Pred. No. 2.4e-200;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                       Minimal function unit; MFU; human; elastin prosthetic.
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                                                                                                                  The present invention relates to a minimal functional unit (MFU) of human elastin polypeptide. This protein is useful in a cosmetic material or a prosthetic material such as prosthetis for blood vessel replacements, for heart valve replacement, tissue replacement, for covering burns, for covering wounds and stents
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                                            Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
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                                                                                                 Claim 1; Fig 1; 39pp; English.
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Db δ d δ qq ò qq ð Db δ

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Human synthetic tropoelastin is susceptible to hydrolytic breakdown of the crosslinks. Such material may be useful in e.g. surgical applications, where the gradual loss of material over time is intended. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 2.4e-200;
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                                                                                                                                                          Tropoelastin; pharmaceutical; surgical
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                                                                                                                       Synthetic human tropoelastin
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   protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
                                                                                                                                                                       KYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAKAAAKAAQFGLVGAAGLGGLGVG
           VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGA
                                                                                                   --VPGALAAAKAA
PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                         AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
                                                                                                                                                 543 GVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAA
                                                                                                                                                                                                                              GLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGA
                                                                                                                                                                                          628 GLGVPGVGGLGGIPPPAAAKKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGA
                                                                                                                                                                                                                                                                                                                                                                                                                       Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New derivatives of human tropoelastin - with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of synthetic human tropoelastin SHEL.
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Homo sapiens.
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      foods and industrial
wrinkle or hand lotions, also as surgical implants, foods and industrice products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTB. The present sequence represents the amino acid sequence of the synthetic human tropoelastin SHEL.
                                                                                                                                                                                                                                                                    61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                                     GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiathritis; osteopathic; antigout; antinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
PGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGAR 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia e
                                                                                                                          akaakygvgtpaaaakaaakaaQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
                                                                                                                                                                                                                                                                     GVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAA
                                                          VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVFGLGVGA
                                                                                                                                                                                           KYGAAVPGVLGGLGALGGVGI PGGVVGAGPAAAAAAAAAAKAAQFGLVGAAGLGGLGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human elastin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the use of an agent that promotes clastin signaling in smooth muscle cells for decreasing or preventing coclusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin polymerisation, increasing F:G actin ratio in a smooth muscle cell; creating or preventing obstructive vascular disease (e.g. restensis), or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells is useful for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis following angioplasty), or preventing censoris. It is also useful in manufacturing a medicament for the treatment or prevention of occlusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 757;
                                              Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasctropic.
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                                                                                                                                                                                                    27-MAR-2003; 2003WO-US009391.
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              tropoelastin protein
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698; Conserv
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                                                                                                                                  WO2003082203-A2
                                                                                                    Homo sapiens.
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Containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that can expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes for targeting in the treatment of the unatoid arthritis; identification of their than a mouse; diagnosis of rheumatoid arthritis; an amammal carry or gene chip, specific for rheumatoid arthritis; argument of collagencarry or gene chip, specific for rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagency of a candidate drug in vitro for the treatment of collagency induced arthritis; and reducing the symptoms associated with collagency of a candidate drug in vitro for the invention have the following activities: immunosuppressive, antirheumatoid, antirheumatory, dermatological, and immunomodulatory. The mompositions of the present invention are useful for antigout, antiritis, lupus, ankylosing spondylitis, fibrositis, fibrositis, fibrosing and treating autoimmune disease or arthritides, such as the immuno disease caused by an infectious agent. This sequence is not shown in the specification. It has been supplied in an electronic format from when The method comprises obtaining a autoimmune disease or arthritides.

Sequence 757 AA;

1; 120 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPCVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 146 180 240 206 266 300 360 386 420 626 326 446 480 506 540 566 567 09 98 568 KYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAKAAQFGLVGAAGLGGLGVG 627 GGVPGAI PGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 27 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKP GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL PGVY PGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGI PGVGPFGGPQPGVPLGY 147 PGVYPGGVLPGARFPGVGVLPGVTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAKF GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAGAR PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKAAK PGVGVGGIPTYGVGAGGFFGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA 567 GVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPGTPSSPRVPGALAAAKAA PGVGVGGI PTYGVGAGGFPGFGVGVGGI PGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA akaakygvgtpaaaaakaaakaaQfGlvpgvgvapgvgvapgvgvapgvglapgvgvapg VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLRAAAGIGAGIPGLGVGVGVPGLGVGA 507 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGA --VPGALAAAKAA Gaps 33; 99.3%; Score 3588.5; DB 7; Length 757; 95.5%; Pred. No. 2.5e-200; ive 0; Mismatches 0; Indels 33; GVPGLGVGAGVPGFGA--Conservative Similarity 698; Query Match Best Local S Matches 698 Н 61 181 267 241 301 327 361 387 447 481 421 qq ₹ g $\stackrel{>}{\circ}$ qq ò 엄 ð g ð g δŏ Ωp à q ₹ g ð g

KYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAAAAAAAAAAAAAAAAGLGGLGVG 687 746 This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, metal or synthetic material, where the surface is coated with the polypeptide, a comprising the polypeptide, a high tensile strength material comprising the polypeptide, a high tensile strength material comprising the polypeptide, a high tensile strength material polypeptide comprising the polypeptide comprising the polypeptide comprising at least three beta sheet/beta turn spructures, (b) a polypeptide consisting essentially of a purton of the polypeptide consisting essentially of a portion of the amino acid sequence of an animal elastin comprising at least three beta sheets/beta turns, (c) a polypeptide consisting essentially of a portion Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns. GLGVPGVGGLGGIPPPAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGA GLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGA fibrous protein; prosthesis; elastin; lamprin; spider silk protein; blood vessel; wound; burn healing; collagen. 190.
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 <li 9 in claim 6" in claim 6" in claim /note= "region specifically claimed 374.-.499 /note= "region specifically claimed 607...717 "region specifically claimed Rothstein S; Location/Qualifiers ADL96420 standard; protein; 731 AA. Human elastin protein fragment. Claim 5; Fig 1B; 17pp; English. 97US-00911364. 99US-00340736. 28-SEP-2001; 2001US-00964662. 96US-0023522P. (first entry) .367 698 CLGKACGRKRK 757 Keeley F, /note= CLGKACGRKRK (ROTH/) ROTHSTEIN A. (ROTH/) ROTHSTEIN S. WPI; 2003-898105/82. US2003166846-A1 KEELEY Homo sapiens Rothstein A, 20-MAY-2004 07-AUG-1996; 07-AUG-1997; 29-JUN-1999; 04-SEP-2003 627 628 688 747 ADL96420; 687 KEEL/) Region Region Region Region RESULT 11 ADL96420 à g ð q

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secondary structure comparison at manufacture.

secondary structure comparison at least three beta sheets/beta turns, where each of the beta sheet/beta turn structures comprises from 3 to about 7 amino acids and the polypeptide is not a maturally occurring fibrous protein. The minimal functional unit (WRU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing. Alternatively the MFU can be co-aggregated with other proteins, for example collagen, to provide prosthesis material that resembles the natural structural materials of the body. The MFU based material is subject to infiltration of cells growing in the patient, including endothelial cells, and the prosthesis can become a permanent living tissue, replacement. The material is more biocompatible than other elastin
                                   at
                             polypeptide consisting essentially of a spider silk protein comprising least three beta sheets/beta turns, a polypeptide having the primary structure of a portion of a naturally occurring fibrous protein and a
comprising at least three beta sheets/beta turns, and (d)
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Sequence 731 AA;

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                                                                                         PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKF
                                                                GGVPGAIPGGVPYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                    FPGALVPGGVADAAAAXKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
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                                 Gaps
                                 33;
DB 7; Length 731;
                                   1; Indels
Score 3580.5; DB Pred. No. 7e-200;
                                   Mismatches
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     99.0%;
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                                       Conservative
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     Query Match
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Claim 1; Fig 1B; 21pp; English.

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beta-sheet/beta-turn structure; fibrous protein; prosthesis;
blood vessel replacement; heart replacement valve; burn; wound; lamprin;
spider sllk; oord; rope; parachute; cosmetic; platelet binding inhibitor;
platelet activation inhibitor; non-thrombogenic; cell infiltration;
non-immunogenic; blocompatible; high tensile strength; elasticity;
                                                                                                                                                                                                                                                                                                                                             Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not naturally occurring fibrous protein.
                                                                                                                     elastin; minimal functioning unit; MFU;
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                                                                                                                                                                                                                                                                                                                 Keeley F, Rothstein
                                                  A.
                                                  ABU08725 standard; protein; 731
                                                                                                                                                                                                                                                                                        & DEV LP.
SPECIALTIES LTD.
                                                                                                                                                                                                                                             99US-00340736.
                                                                                                      Human elastin mature protein.
                                                                                                                                                                                                                                                              96US-0023522P
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                                                                                      (first entry)
WPI; 2003-391056/37.
                                                                                                                                                                                                                                                                                       (HSCR-) HSC RES
(PROT-) PROTEIN
                                                                                                                                                                                                                                                                                                                 Rothstein A,
                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                              29-JUN-1999;
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07-AUG-1997;
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                                                                                                                                                                                                                              03-DEC-2002.
                                                                                     25-JUN-2003
                                                                                                                                                                          plasticity.
          721
                                                                     ABU08725;
                                   RESULT 12
                                             ABU08725
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The invention describes a polypeptide (I) comprising a minimal functioning unit (MFU) which is present in the sequence of human elastin cfunctioning unit (MFU) which is present in the sequence of human elastin least three beta-sheet/beta-turn structures, and at least one aminon acid residue that participates in cross-linking, and not construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel control of the conformation of the co immunogenic, thus providing a truly biocompatible material. MFUs modeled on lamprin and other fibrous proteins can be used to make a variety of materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human

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374. .499 /note= "MFU-1 polypeptide"

WO9805685-A2

12-FEB-1998

Location/Qualifiers

Homo sapiens

Protein

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                                                                                                                  GGVPGAIPGGVPGGVFYPGAGIGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                 PPGALVPGGVADAAAAXKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
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                                                                                             GGVPGAIPGGVPGGVFYPGAGLGALGGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                          33;
                                                 DB 6; Length 731;
elastin on which the MFU peptides of the invention are based
                                                                         2; Indels
                                                Score 3578.5; DB 6;
Pred. No. 9.2e-200;
0; Mismatches 2;
                                               99.0%;
                                                                     Conservative
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                                        Query Match
Best Local Similarity
Matches 696; Conser
                      Sequence 731 AA;
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New non-natural polypeptide with multiple beta-sheet, beta-turn structures - particularly based on human elastin, useful for coating prostheses, as wound dressings, etc., allows ingrowth of cells.

Claim 5; Fig 1B; 39pp; English.

Rothstein SJ;

ĒΜ,

Keeley

Rothstein A,

WPI; 1998-145551/13.

HOSPITAL FOR SICK CHILDREN.

PROTEIN SPECIALTIES

(PROT-) (HOSP-)

97US-00911364.

97WO-CA000560 96US-0023552P

07-AUG-1997; 07-AUG-1996; 07-AUG-1997;

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This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 1 seat 1 seat. Speta-structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides are self-aligning peptides can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides are self-aligning peptides comparing the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, coming the same primary structure. They can be used in cosmetic, elastic or high-tensile strength materials, e.g. ropes or parachute cord.

They are based on the MFU allow penetration of endothelial cells, so become permanent, living, tissue replacements. The MFU polypeptides have the elected blocompatibility than known elastin-based materials. They are well archive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider
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Pred. No. 2.2e-199;
0; Mismatches 0;
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95.3%;
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MFU-1; minimal functional unit; elastin; human; fibrous protein; beta-sheet; coating; wound dressing. Human elastin containing non-natural polypeptide MFU-1 sequence.

AAW46315 standard; protein; 730 AA.

RESULT 13 AAW46315 23-JUL-1998

AAW46315

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NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
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                  pgrgpgvvgvpgagvpgvgvpgagipvvpgagipgaavpgvvspbaaakaaakaakraak 360
                                                                                                            pcycyciciptycycaccepercycyccipcyacypsyccypcyccybcyclispeachaaa 420
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GAGAAGVI.PGVGGAGVPGVPGAI.PGI.GGI.AGVGTPAAAAAAAAAAKAAKYGAAAGI.VPGG
                                             PGFGPGVVGVPGAGVPGVFGAGIPVVPGAGIPGAAVPGVVSPBAAAKAAAKYGAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE40132 standard; protein; 711
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2001US-0310291P.
2001US-0310544P.
2001US-0310951P.
2001US-0311992P.
2001US-0311979P.
2001US-031292P.
2001US-0313201P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2002; 2002WO-US024483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue typing; hūman; NOV
                                                                                                                                                                                                                                                                                                                                                                     698
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07-AUG-2001; 2
08-AUG-2001; 2
09-AUG-2001; 2
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17-AUG-2001;
17-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001;
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprocetrive, nootropic, antiparkinsonian, attiastimatic and synaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosolarosis, hypertension, cancer, obesity, diabetes, AIDS, multiple solerosis, preversus-host disease, Alzhaimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as butilised in gene therapy, chromosome mapping, tissue typing, hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leiter MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
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                                                                                                                                                                                         19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373825P.
19-APR-2002; 2002US-0373899P.
23-APR-2002; 2002US-0374632P.
07-JUN-2002; 2002US-0386971P.
01-AUG-2002; 2002US-0386971P.
           2001US-0313702P.
2001US-0314031P.
2001US-031466P.
2001US-03156403P.
2001US-0315853P.
2001US-032394P.
2001US-0340233P.
2001US-0340233P.
2002US-0354591P.
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Best Local Similarity
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Alsobrook JP,
Smithson G;
                20-AUG-2001;
21-AUG-2001;
23-AUG-2001;
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29-AUG-2001;
17-SEP-2031;
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05-FEB-2002;
19-MAR-2002;
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                    AAAKFGAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKYGAAAG
                                                                                         327 LVPGGPGFGPGVVGVPGAGVPGVPGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAA
                                                                                                                               KYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEA
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Tropoelastin, elastin, elastic fibre, smooth muscle cell proliferation, smooth muscle cell differentiation, smooth muscle cell migration, smooth muscle cell function, atherosclerosis, restenosis, aneurysm, vascular bypass graft stenosis; transplant arteriopathy, dissection, hypertension; transplant arteriopathy. SVAS;

WO200050068-A2 Homo sapiens

31-AUG-2000

2000WO-US002526 28-FEB-2000;

26-FEB-1999;

UTAH RES FOUND. UTAH) UNIV

Li DY; Keating MT,

WPI; 2000-533134/48.

Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.

English 19pp; Example 3; Page 46;

The present sequence represents a human elastin. Peptides derived from

AAB08631 standard; peptide; 730 AA

AAB08631 ID AAB0 XX

elastin are used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprishing; inhibiting the proliferation of smooth muscle cells in vivo; snd regulating the differentiation of smooth muscle cells in vivo; and regulating the migration of smooth muscle cells in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized by diminished capacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vasculat bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy 120 146 180 240 366 300 09 326 360 386 420 446 474 506 534 999 594 626 654 98 27 GGVPGAIPGGVFGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 1 GGVPGAIPGGVPGGVFYPGAGLGALGAGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKF 207 PIKABKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAKAAAKF GAGAAGVI.PGVGGAGVPGVPGAI.PGI.GGI.AGVGTPAAAAAAAAAAAKAAKYGAAAGI.VPGG GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG 567 GLGVGAGVPGLGVGAGVPGRGAVPGALAAAKXGAAVPGVLGGLGALGGVGIPGGVVG 595 AGPAAAAAAAAAAAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAA PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAG1PGVGPFGGPQPGVPLGY PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKYGAR PGVGVGGVGGIPTYGVGAGGFPGFGVGVGGVGGVPGVGGVPGVGGVPGVGGVPGAAAA 387 PGVGVGGIPTYGVGGFPGFGVGGGFPGVAGVPGVGGVPGVGGVPGVGGVPGVGGSPEAQAAAA AKAAKYGVGTPAAAAKAAAKAAQF-----GLVPGVGVAPGVGVAPGVGVAPGVGLAPG VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGI PGLGVGVGVP GLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGI PGGVVG Gaps 24; Length 712; Indels GLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK Score 3485; DB 3; Pred. No. 2.4e-194; 0; Mismatches 1; 96.48; 679; Conservative Similarity Sequence 712 AA; 181 447 121 267 327 535 Query Match 241 301 361 421 475 655 Best Local 684 Matches RESULT 16 \$ g ò g ò g ò d à Ob $\stackrel{>}{\circ}$ 셤 ò ΩD à g à g δ d à g à

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09-AUG-2001; 2
13-AUG-2001; 2
16-AUG-2001; 2
17-AUG-2001; 2
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20-AUG-2001; 2
21-AUG-2001; 2
23-AUG-2001;
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03-AUG-2001;
07-AUG-2001;
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                                                                 Tropoelastin, elastin, elastic fibre; smooth muscle cell proliferation, smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell midration; atherosclerosis; restenosis; aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; sVAS; hypertension; transplant arteriopathy.
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                                                                                                                                                                                                                                                                                                                                                                    Elastin based compositions useful for treating atherosclerosis,
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                                            Fusion protein comprising human elastin and c-myc
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Pred. No. 2.4e-194;
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96.4%;
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Best Local Similarity
Matches 679; Conserv
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                                                                                                                                                                       Unidentified.
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                                                                                PGFGPGVVGVPGAGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKYGAR
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GAGAAGVI.PGVGGAGVPGAPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGI.VPGG
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2001US-0312892P.
2001US-0313201P.
2001US-0313415P.
2001US-0313643P.
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2001US-0310291P.
2001US-0310544P.
2001US-0310951P.
2001US-0311292P.
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2001US-0314031P.
2001US-0314466P.
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N-PSDB; AAX27705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidabelic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and preventing NOVA-associated disorders including cardiomyopathy, preventing NOVA-associated disorders including cardiomyopathy, sclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple atherosclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                      New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing
                                                                                                                                                                              Rekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK, Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ; Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW; Guo X, Zhong M, Gerlach VL, Hialt T, Rastelli L, Spytek KA; Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ; Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3366; DB 7; Length 692;
Pred. No. 1.8e-187;
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                                  : 2001US-0323994P.
: 2001US-0340233P.
: 2002US-0354591P.
: 2002US-0365478P.
                       2001US-0322716P.
                                                                              2002US-0373814P
                                                                                                   2002US-0373989P.
                                                                                          2002US-0373825P
                                                                                                                           2002US-0386971P
                                                                                                                                     2002US-00210172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.1%;
93.8%;
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                                                                                                                                                         (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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N-PSDB; ADE40133
                                                                                                                                                                                                                                                                                                                                            pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 692 AA;
                       -2001;
-2001;
                                                      05-FEB-2002;
                                             14-DEC-2001;
                                                                                                                                    01-AUG-2002;
                                                                              19-APR-2002;
                                                                                                    19-APR-2002;
                                                                                                            23-APR-2002;
                                                                                        19-APR-2002;
                                                                                                                        07-JUN-2002
                                                                                                                                                                                                                                                  Smithson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a derivative or variant of human tropoelastin (hTB) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical,
                                    349 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPGVPGVPGVGGVPGVGTSPEAQAAAA
                                                                                                                                                                                                                                                                                     409 AKAAKYGVGIPAAAAAKAAAKAAQFALLNIAGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVGLAPG
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                                                                                                                  PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                                                                                                                                                                                                                    AKAAKYGVGTPAAAAKAAAKAAQF-----GLVPGVGVAPGVGVAPGVGVAPGVGTAPG
                                                                                                                                                                                                                                                                                                                                                                                                          469 VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macromolecular binding properties, useful e.g. as surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 GLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 GLGGVLGGAGQFFLGGVAARPGFGLSPIFPGGACLGKACGRKRK 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tropoelastin derivative SHELdeltamodified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01303 standard; protein; 660
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Ishii S; , Tamechika I;

Otsuki T, Wakamatsu A, Sato H, Ish Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y;

(REAS-) RES ASSOC BIOTECHNOLOGY

Sugiyama T, J, Isono Y, Yoshikawa T, 2003-723558/69.

Yamamoto J,

Isogai

Seki N,

12-APR-2002; 2002EP-00008400. 22-MAR-2002; 2002JP-00137785

24-SEP-2003

Homo sapiens.

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959
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pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
wrinkle or hand lotions, also as surgical implants, foods and industrial
products. The hybrid protein have controllable 6Ag-binding properties,
depending on presence or absence of a specific fragment, designated
peptide 26A, from hTE. The present sequence represents a human
tropoelastin derivative SHELdeltamodified
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                                                                                                                                                Gaps
                                                                                                                                               47;
                                                                                                                        Length 660;
                                                                                                                                                Indels
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                                                                                                                        DB 2;
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                                                                                                                      Score 3248.5; DB 2
Pred. No. 1.1e-180;
3; Mismatches 8;
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                                                                                                                           89.98;
91.78;
                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 644; Conservative
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                                                                                                   Sequence 660 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM0509-ADM06201 encoded by the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKAAKYGVGTPAAAAKAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGVPGAIPGGVPYPGAGLGALGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are useful as pharmaceutical agents. The present sequence represents protein sequence of the invention.
                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gsvpgalpggvpggvpypgaglgalgggalgpggkplkpvpgglagaglg-
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Pred. No. 8.5e-180;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2477; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sch 89.4%; similarity 90.8%; 634; Conservative
                                                                                                                                                                                                                                          WPI; 2003-723558/
N-PSDB; ADM01349.
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                                                                                                                                                                                                                                                                                                                                            Claim 1;
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human; gene therapy; diagnostic marker; pharmaceutical.

SEQ ID NO:2477

of the invention

Human protein 20-MAY-2004

(first

Length 870;

84.0%;

Local Similarity

Query Match

Sequence 870 AA;

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540
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                   VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGA
                                  446 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLKAAAGLGAGIPGIGVGVGVGVGVGG
                                                       541 GVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAA
                                                                                            601 AAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                               novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                         Novel protein (useful for identifying genetic disorders) #682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                             626 GGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGWKRK 663
                                                                                                                                  661 GGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W, Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;
AKAAKYGVGTPAAAAAAAAAAAAQFGLV-
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                                                                                                                                                                                                   ADE08527 standard; protein; 870
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2002US-0372381P.
2002US-0372615P.
2002US-00128558.
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en R, Xu C,
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2001US-0339453P.
2002US-0365091P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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14-MAR-2002;
                                                                                                                                                                                                                                                                                                           Unidentified
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24-APR-2002;
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cell regeneration, membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAPGIGFGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVFGLGVGGGVPGLGVG
                                                                                                                                         -----GVGLPGVYPGGV
                                                                                                                                                                                   226 LPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLP
                                                                                                                                                                                                                         GGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAKFGAGAAGVL
                                                                                                                                                                                                                                                                                                         346 PGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGGPGFGPGVV
                                                      19 GAGLGALGGGALGPGGKPLKP------VPGGLAGAGLGAGLGAFPAVTFPGALVPG
                                                                                                            GVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGV
                                                                                                                                                                    LPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLP
                                                                                                                                                                                                                                                                                249 PGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAAAAAAGLVPGGPGFGPGVV
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                                                                                                                                                                                                                                                   286 GGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAAKFGAGAAGVL
                                                                                                                                                                                                                                                                                                                                       GVPGAGVPGVGGAGI PVVPGAGI PGAAVPGVVSPEAAAKAAAKAAAKYGARPGVGVGGI
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                                                                                                                                                                                                                                                                                                                                                                                              369 PTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAAAAKYGV
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                                Gaps
                             Indels 126;
                                11;
Score 3038; DB 7;
Pred. No. 2.3e-168;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQFPLGGVAARPGFGLSPIFPGG---ACLGKACGRK
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                             Conservative
                                                                                                                                        200 GVADAAAAYKAAKA
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                          616;
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                           Matches
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.

for tissues

New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tin which the corresponding protein is preferentially expressed.

Claim 20; SEQ ID NO 1593; 1177pp; English

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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                    342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 AAAAKAAAKAAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVL 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             588
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                                       300
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                                                                                                                                                                                                                                                   -----EAQAAAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                              481 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGA
                                                                               223 GAGAAGVI.PGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAKAAKYGAAAGI.VPGG
                                                                                                                        PGFGPGVVGVPGAGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKYGAR
                                                                                                                                                                PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGAR
                                                                                                                                                                                                                                                                                                                       163 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKF
                                       GAGAAGVI.PGVGGAGVPGVPGAI.PGI.GGI.AGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG
                                                                                                                                                                                                            PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAKAAKY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human tropoelastin derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GVAARPGFGLSPIFPGGACLGKACGRKRK 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK 698
                                                                                                                                                                                                                                                          343 PGVGVGGIPTYGVGAGGFPGFGVGVGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel collined is a polypeptide encoded by the polynucleotide or its partial peptide, immunologically assaying the polypeptide or peptide or its partial peptide, immunologically assaying the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide or the polynucleotide by contexting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding conversable manner and an antisense polynucleotide. The oligonucleotide in an expressible manner and an antisense polynucleotide, or as a probect or susful as paramacutical agents and many disease-related proteins are useful as pharmacutical agents and many disease-related proteins of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, disease-related proteins, disease-related proteins and genes concoding them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, concorred presented is a protein of the invention. Note treat diseases. The common disease for the invention to treat diseases.
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                                                                                                                                                                                                                                                                                                                         Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
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RES ASSOC BIOTECHNOLOGY.
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84.5%;
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2002US-00350978
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Seki N, Yoshikawa T,
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                                                                                                                                                                                                       05-NOV-2001;
25-JAN-2002;
                                       Homo sapiens
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                                                                                                                        07-MAY-2003
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so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be contact the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative competitive inhibition of protease activity. The tropoelastin derivative derivatives, and other polypeptides containing tropoelastin derivative. The competition of protease susceptibility sites, are useful in human or veterinary and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidominetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or protease activity that causes blood clotting
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                                                                                                                                                                                                                                                                                                                                                                                                          79.4%; Score 2869; DB 3; Length 571; 99.6%; Pred. No. 1e-158; ive 0; Mismatches 2; Indels
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AAY69135 standard; protein; 515 AA.

RESULT 23

(first entry)

30-MAY-2000

AAY69135;

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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated tropoelastin derivatives of the invention a subsequence has been mutated to that susceptibility to proteclysis is subsequence has been inserted so that susceptibility to proteclysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide contact with serum or wound exudate. The tropoelastin derivative protease-susceptibility sites, are useful in human or veterinary and for inducing chemotaxis. They are also useful for proliferation or and for inducing chemotaxis. They are also useful for proliferation or competition, particularly of smooth muscle cells, epithabial or growth inhibition, particularly of smooth muscle cells, epithabial or growth inhibition, particularly of smooth muscle cells, epithabial or endothelial cells, fibroblasts, osteoytes, chondrocytes and platelets. Ce protecting against lung damage caused by elastin, for inhibiting or protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                  Tropoelastin, derivative, proteolysis, protease, antiwrinkle, hand lotion, bulking agent, chemotaxis, proliferation, growth inhibition, peptidomimetic, lung damage, elastin, cancer, metastasis, blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                              derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FPGALVPGGVADAAAAXKAAKAGAGLGCVPGVGGLGVSAGAVVPQPGAGVKPGKVPGKVPGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAGAAGVI.PGVGGAGVPGVPGAI.PGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGI.VPGG
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  Amino acid sequence of a human tropoelastin derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 131-133; 136pp; English
                                                                                                                                                                                                                                                                         98AU-00004723.
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                                                                                                                                                       WO200004043-A1
                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                           17-JUL-1998;
                                                                                                                                                                                            27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell growth.
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a control of that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity as a compound to small molecule that regulates the solivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
                                                                                                                                 480
                                                                                                                                                             AKAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVGVAPG
                                                                                   two or more isolated polypeptides, useful for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  in; neuronal tissue; gene therapy; spinal segmental nerve injury; constriction injury; CCI; spared nerve injury; SNI; Chung.
                 AKAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
PGFGPGVVGVPGAGVPGVPGAGI PVVPGAGI PGAAVPGVVSPEAAAKAAAKAAKYGAR
                                                                PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGTSPEAQAAAA
                                                                                                                                                                                                   VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR
                                                                                                                                                                                                                           VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2524
                                                                                                                                                                                                                                                                                                                      ADE56670 standard; protein; 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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(FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592
pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating plain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 AGAĞVPGFGAĞAVPGSLAASKAAKYGAAGGLGGPĞGLĞĞPĞGLĞĞPGGFGGPGGLĞÖVPĞ
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                                                                                                                                                                                                                                                                                                                                                      90 GAGLSY--ASRPGGVLVPGGGAGAAAXKAAAKAGAGLGGIGGVPGGVGGVPGAVGVG
                                                                                                                                                                                                                                                                                                                                                                                                                          148 GVPGAVGGIGGIGGLGVSTGAVVÞQLGAGVGAGGKÞGKVÞGVGLPGVYÞGGVLÞGTGARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYTTGKL.PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAKAAAKFGAGAAGVL.PGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYTNGKLPY-----GVAGAGGKAGYPTGTGVGSQ-AAVAAAKAAKYAGAGGGGVLPGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKYGAAAGLVPGGPGFGPGVGVPGA
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                                                                                                                                                                                                                                                                        --VPGGLAGAGL
                                                                                                                                                                                                                                                                                                                                                                                                ----GGLGVSAGAVVPQPGAGV----KPGKVPGVGLPGVYPGGVLP--GARF
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                                                                                                                                                                                                                                         219;
                                                                                                                                                                                                            Length 864;
                                                                                                                                                                                                            Score 2315.5; DB 7; Length
Pred. No. 1.8e-126;
26; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                    GAGLGAFPAVTFPGALVPGGVADAAAAYK-AAKAGAGLGGVPGV-
                                                                                                                                                                                                                                                                        GGVPGAIPGGVPGGVFYPGAGL-GALGGGALGPGGKPLKP
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nes 529; Conservative
                                                                                                                                                                                  Sequence 864 AA;
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This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by AAB88317
CAAF62232 - AAF62235 which are used to isolate the CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can the used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the production of the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes of in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The gainst them and in assays to identify modulators (agonists and antagonists of expression and activity. The antibodies and antagonists of activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists of activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and detecting the presence of the polypeptides in samples (e.g. by enzyme conting the presence of the polypeptides in samples (e.g. by enzyme the turbed architits and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.
                                                                                                                                                                                                                                                                                           Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T,
                                                                                                                                                                                                                                                     Human membrane or secretory protein clone PSEC0191
      ---GGACLGKACGRKRK 698
                      829 GLGVGGKPPKPYGGALGALGYQGGGCFGKSCGRKRK 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai Y,
                                                                                                                                  AAB88422 standard; protein; 472
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2000JP-00118775.
2000JP-00183766.
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           EP1067182-A2
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61 FPGALVPGGVADAAAAYKAAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAAKYGAAAGLVPGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPBAAKAAAKYGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 PGFGPGVVGVPGAGVPGVGGVPGAGIPVVPGAGIPGAAVPGVVSPEAAKAAAKAAKAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVGVAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGIGVGVGVPGLGVGT
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GVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGI
                                                                                                                                                                                                                                                                                                                                                                                                ---GB---
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/note= "polymer repeat block sequence"
                                                                                                                                                           -LGGVGI
                                                                                                                                                                                                                                                                                                                                                                                             --- PGGVVGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR80253 standard; peptide; 988 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US002772,
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1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFFAVT 60

5.

Gaps

Indels 226;

Score 1679; DB 4; Length 472; Pred. No. 8.8e-90; 3; Mismatches 3; Indels 22.

46.4%;

alternating blocks of fibroin and elastin ice e.g. a suture to keep separated viable form a device e.g. a comprising Protein polymer units - used to

Example 1; Page 27-30; 46pp; English.

The sequences represented by AAR80251-R80257 are polymers constructed of repeating blocks of fibroin-like (see AAR80249) and elastin-like (see AAR80250) units. This sequence contains 13 repeats of a block consisting of 8 alastin-like repeats followed by 6 fibroin-like repeats. The DNA sequences encoding these polymers were inserted into plasmids which were used to transform E.coli strain EC3. The polymers could then be isolated from the fermented strains BC3. The polymers could then be isolated to polymers are used to form a device (such as a suture, pin, thread, gel or polymers are used to form a device (such as a suture, pin, thread, gel or film) to keep separated viable tissue together. By varying the the ratio of the two repetative units, and by altering the lengths of the blocks of cach of them, the tensile properties of the polymer can altered moderatly. By reducing the number of repeating units of this sequence, or the or resorption can be achieved. Of the polymers, SELPO (see AAR80251) and the fastest resorption rate. The SELPA (see AAR80255) and SELP5 (see AAR80255) polymers showed intermediate resorption. No data was given for three polymers showed intermediate resorption. No data was given for (see AAR80257)

AA; Sequence 988

527 GAGAGSVPGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGGAGAGSG 579 235 KAAAKFGAGAAGVLPGVG--GAGVP--GVPG-AIPGIG----GIAGVGTPAAAAAAAAA 285 351 338 411 PGVVSPEAAKAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGV----AGV 394 467 PSVG----GVPGVG----GVPGVGISPEAQAAAAKAAKYGVGTPAAAAAKA----AAK 441 501 105 149 48 69 442 AAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAA ---- PĠVĠĠĀGĀĠĀGĀGSGAGAGSGAGAGSGAGAGSGAGAGSVPĠVĠV---PĠVĠVP-241 GVGVPGVGVPGVGVPGVGVPGVPGVGVPGVGSAGAGSGAGAGSGAGAGSGAGAGS 293 GAGAGSGAG-AGSVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGAGAGSG -GPGFGPGVVGVPGAGVPGAGIP--VVPGAGIPGAAV 352 AGAGSGAGAGSGAGAGSGAGAGSVEVGVVEVGVVBEVGVPEVGVBEVGVBTGVGV pgygypgyggagagagagagagagaga----gagsgagagagagagsypgygygy ---IPGVGPFGGPQPGVPL LGAGLGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ-GYPIKAPKLPG----GYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAA ----GKPLKPVPGGLAGAG ----PGAGVKPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGV Gaps Indels 178; Length 988; 4e-59; 248; DB 2; GVPG-AIPG-GVPG----GVFYPGAGLGALGGGALGPG-Mismatches 32.0%; Score 1155; 41.6%; Pred. No. 4e-KPKAPGVGGAFAG------49; KAAKYGAAAGLVPG----Conservative Local Similarity 338; 468 286 339 412 395 49 189 N 10 106 179 Query Match Best Loca Matches q g δ g à Dp ð g 셤 q à 임 ò Ω δ δ à

Claim 19; Page 22; 32pp; English.

drug delivery

that

681 GAĠSŸPGVĠVPĠVĠVPĠVĠVPĠVĠVPGVGVPĠVĠVPGVĠVPGVGĀGĀGĀGSGAGĀĠSĠAGĀ 740 611 657 composition comprising a repetitive polymer containing alternating sks of sequences that promote protein crystallization and sequences: are elastin, collagen or keratin-like elements, useful for in vivo Protein crystallisation; elastin; collagen; keratin; controlled release; 612 OFGLYGAAGLGGLGYGGLGYPGYG----GLG----GIPPAAAAKAAKYGAAGLG---pgfgavpgalaaakaakygaavpgvlgglgalggvglpggvvgagpaaaaaakaaakaa ---vpgv-ggagagsgagagsg-agagsgagagsgagagsga polymer block amino acid sequence. 685 GSGAGAGSGAGAGSVPGVGVPGVGVPG 773 -GVLGGAGQFPLGGVAARPGFGLSPI-FPG Ā. ABP53474 standard; protein; 988 97US-00806029 97US-00806029 ER; (first entry) Cappello J, Stedronsky (CAPP/) CAPPELLO J. (STED/) STEDRONSKY E R. Protein polymer SELP7 WPI; 2002-681318/73. physical dimension. US2002045567-A1. PGVG 24-FEB-1997; 24-FEB-1997; 20-NOV-2002 18-APR-2002. blocks of Synthetic ABP53474; 552 640 658 741 RESULT 27 ABP53474 à 원 ò q ð 음

The present invention describes a composition (C1) comprising: (a) a protein polymer of at least 15kDa which comprises alternating blocks of protein crystallisation, and an amino acid sequence which promotes croprotein crystallisation, and an amino acid sequence which is an elasting protein crystallisation, and an amino acid sequence which is an elasting composition crystallisation, and an amino acid sequence which is an elasting composition dependent, a collagen-like element or a keratin-like element, and (b) like element, a collagen-like element or a keratin-like element; and (b) composition acquires a non-liquid comprision comprision comprision of administering of the biologically active substance to a localized site in vivo, comprising administering composition is used for the controlled release of biologically active compounds in vivo. It can also be used to alter the physical dimensions compounds in vivo. It can also be used to alter the physical dimensions compounds in the present sequence represents a protein polymer block amino acid sequence from the present invention

Sequence 988 AA;

---IPGLGV-GVGVPGLGV-GAGVPGLGV-GAGV 551

502 AKSAAKVAAKAQLRAAAGLGAG-

46; Gaps 32.0%; Score 1155; DB 5; Length 988; .larity 41.6%; Pred. No. 4e-59; Conservative 49; Mismatches 248; Indels 178; Best Local Similarity Matches 338; Conserv Query Match

us-09-743-818a-5.rag

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234
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                                                                          -----PGAGVKPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGV 149
                                                                                                                                                           ----IPGVGPFGGPQPGVPL 178
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    GKPLKPVPGGLAGAG 48
                        ĠVPĠVGVPĠVĠVGVPĠVGVPĠVĠVPGVĠGAGAGAGAGAGAGAGAGAGAGAGA
                                                                                                                                                                                                         GYPIKAPKLPG----GYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAA
                                                                                                                                                                                                                                49 LGAGLGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ-
                                                                                                                  235 KAAAKFGAGAAGVLPGVG--GAGVP--GVPG-AIPGIG----GIAGVGTPAAAAAAAAA
                                                                                                                                                                                                                                                                                                             286 KAAKYGAAAGLVPG-----GPGFGPGVVGVPGAGVPGVGVPGAGIP--VVPGAGIPGAAV
                                                                                                                                                                                                                                                                                                                                                                                                                 395 PSVG----GVPGVG----GVPGVGISPEAQAAAAAAAKAGVGTPAAAAAKA----AAAK
                                                                                                                                                                                                                                                                                                                                                               PGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFRGVGVGGIPGV----AGV
                                                                                                                                                                                                                                                                                                                                                                                       412 PGVGVPGVGGAGAGSGAGAGSGAGAGSGA----GAGSGAGAGSGAGAGSVPGVGV
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 ---GVFYPGAGLGALGGGALGPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GVLGGAGQFPLGGVAARPGFGLSPI-FPG 685
 GVPG-AIPG-GVPG-
                                                                                                                                                     150 KPKAPGVGGAFAG-
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Conservative
       Local Similarity
nes 345; Conserv
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Query Match
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          Best Loca
Matches
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                                                                                                                                                                                                                       à
                                                                                                                                                                                                        Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk;
polymer; E.coli; EC3.
                                                                                  GSGAGAGSGAGAGGAGSVPGVGVPGVGVPG 773
                                                                                                                               AAR80252 standard; peptide;
                                                                                                                                                                    (first entry)
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Polymer SELP8

AAR80252;

RESULT 28 AAR80252 Synthetic.

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The sequences represented by AAR80251-R80257 are polymers constructed of repeating blocks of fibroin-like (see AAR80249) and elastin-like (see AAR80250) units. This sequence contains 13 repeats of a block consisting of 8 elastin-like repeats followed by 4 fibroin-like repeats. The DNA coll strain Eds. The polymers could then be isolated to used to transform E. coll strain Eds. The polymers could then be isolated from the fermented strains by standard centrifugation techniques. The polymers are used to form a device (such as a suture, pin, thread, gel or from the sep separated viable tissue together. By varying the the ratio of the two repetative units, and by altering the lengths of the blocks of each of them, the tensile properties of the polymer can altered moderatly. By reducing the number of repeating units of this sequence, or moderatly. By reducing the number of the polymer sation (see AAR80251) had the fastest resorption rate. The SELP4 (see AAR80255) and SELP5 (see AAR80255) polymers showed no resorption after seven weeks. The other three polymers showed intermediate resorption. No data was given for SELP6 (see AAR80257)
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                                                                                                                                                                                                                                                                                                                                Protein polymer comprising alternating blocks of fibroin and elastin
units - used to form a device e.g. a suture to keep separated viable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IPGVG--PFGGPQPGVP-LGYPIKAPKLPGGYGLPYTTGKLPYGYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 6.4e-59;
48; Mismatches 228; Indels 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 KPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGVKPKAPGVGGAFAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 832
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                 1. .64
/note= "polymer repeat block sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.8%; Score 1150.5; 44.5%; Pred. No. 6.4e
                                                                                                                                                                                                                     (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 25-27; 46pp; English.
   Location/Qualifiers
                                                                                                                                                  95WO-US002772
                                                                                                                                                                                    94US-00212237
                                                                                                                                                                                                                                                                                              WPI; 1995-328270/42.
                                                                                                                                                                                                                                                                                                                                                                       tissue together
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 832 AA;
                                                                                                                                                                                  11-MAR-1994;
                                                                       WO9524478-A1
                                                                                                           14-SEP-1995
                                                                                                                                                                                                                                                         Cappello J;
               Peptide
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                                                                                                                                                                   GAAVPGV-LGGLGALG----G
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                                                                                                  AKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGTGP
                           ---GAGAGSVP
                                                                           --GAGSGAGAG
                                                                                                                                                    -GAGVP
                                                                                                                                                                                                                                                                                                    ---GIPPAAAAKAAKYGAAGLGGVLG---GAGQFPLGGVAARPGFGLSPI-FPG
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                                                                                                                                                    GGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGV-GVGVPGLGV-GAGVPGLGV-
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STEDRONSKY E
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biologically active substance to a localized site in vivo, comprising administering C1, where the biologically active substance is delivered from the non-liquid to the localized site; and (2) altering the physical dimensions of a body tissue of a mammal, comprising administering a C1. The composition is used for the controlled release of biologically active compounds in vivo. It can also be used to alter the physical dimensions of a body tissue. The present sequence represents a protein polymer block amino acid sequence from the present invention
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                                                                                                                                                                                                                                                               56 FPAVIFPGALLVPGGVADAAAAXKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ----PGAGV 110
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                                                                                                                                                                                                                                                                                          ------IPGVG--PFGGPQPGVP-LGYPIKAPKLPGGYGLPYTTGKLPYGYG-
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                                                                                                                                                        Length 832;
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                                                                                                                                                        Score 1150.5; DB 5;
Pred. No. 6.4e-59;
48; Mismatches 228;
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                                                                                                                                                           31.8%;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                   GVPG-AIPG-GVPG-
                                                                                                                                                                           Similarity
                                                                                                                                   Sequence 832 AA;
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at Local Sum.
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AAR80251;

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The sequences represented by AAR80251-R80257 are polymers constructed of repeating blocks of fibroin-like (see AAR80249) and elastin-like (see AAR80250) units. This sequences contains 18 repeats of a block consisting of 8 elastin-like repeats followed by 2 fibroin-like repeats. The DNA sequences encoding these polymers were inserted into plasmids which were used to transform E.coli strain EC3. The polymers could then be isolated from the fermented strains by standard centrifugation techniques. The polymers are used to form a device (such as a suture, pin, thread, gel or polymers are used to form a device (such as a suture, pin, thread, gel or film) to keep separated viable tissue together. By varying the the ratio of the two repetative units, and by altering the lengths of the blocks of each of them, the tensile properties of the polymer can altered moderally. By reducing the number of repeating units of this sequence, or by increasing the number of units of the elastin like repeat, a faster rate of resorption can be achieved. Of the polymers, this sequence had the fastest resorption rate. The SELP4 (see AAR80255) and SELP5 (see BAR80257) and SELP5 (see BAR80257) and SELP5 (see BAR80257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein polymer comprising alternating blocks of fibroin and elastin units - used to form a device e.g. a suture to keep separated viable
                                                                                      Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk; polymer; E.coli; EC3.
                                                                                                                                                                                                                       /note= "polymer repeat block sequence"
                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEIN POLYMER TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 22-24; 46pp; English.
                                                                                                                                                                                    Location/Qualifiers
1. .52
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                     (first entry)
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                                                     Polymer SELPO
                                                                                                                                                                                                                                                                                                                                                                     11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                  10-MAR-1995;
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114 ĠVPĠVGVPĠVĠVPĠVGVPĠVĠVPĠVĠVPGVĠAGAĠSGAGAGSVPGVGVPGVGVPGVGVP 173 81 KAGAGLG--GVPGVGGLGVSAGAVVPQPGAGVKPG-KVPGVGLPGV-YPGGVLPGARFPG 136 137 VGVLPGVPTGAGVKPKAPGVGGAFAG-----IPGVGPFGGPQPGVPL-GYPIKAPKLP 188 -----GKPLKPVPG-GLAGAGLGAFPAVTFPGALVPGGVADAAAYKAA Gaps Indels 217; DB 2; Length 936; 31.5%; Score 1139.5; DB 2; 41.7%; Pred. No. 3.1e-58; Live 44; Mismatches 228; 2 GVPG-AIPG-GVPG----GVFYPGAGLGALGGGALGPG Matches 350; Conservative Similarity 34 Query Match Local ð 셤 ð qq

226 PQAAAAAAAAKKGAGAAGVLPGVG--GAGVP--GVPG-AIPGIG----GIAGVGTPA 276 605 376 GGFPGFGVGVGGIPGVAGVPSVG----GVPGVG----GVPGVGISPEAQAAAAKAAKYG 427 487 658 545 705 GV-GAGVPGFGAVPGALAAAKAAKYGAAVPGV-LGGLGALG----GVGIPG-GVVGAG-P 597 GLGVGGLGVPGVGGLGGI 640 694 881 509 GAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVPGVGV------PGVGVPGVGVPGVGG 277 AAAAAAAAKAAKYGAAAGLVP--GGPGFG-PGV----VGVPGAGVPGVGVPGAGIP---------VVPGAGIPGAAVPGVVSPEAAKAAAKAGARPGVGVGGIPTYGVGA GVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGV-GVGVPGLGV-GAGVPGL 428 VGTPAAAAAKAAAAFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGLAPGVGVAPGV 641 PPAAAAKYGAAGLG----GVLG-GAGQFPLGGVAARPGFGLSPIFPGGACLGKACG G----GYGLPYTTGKLPYGYGPGGVAGAAGKAGYP-598 AAAAAAKAAAKAAQFGLVGAAGLG----659 GV-PGVGGAGAGSGA----327 488 546 Ωp $\stackrel{>}{\circ}$ Dp g ò à ò qq à g g ö ò g ð qq ò qq δ g

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                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                               on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
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23-JUL-1998 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated application derivative SHELIZE-36
Ade44977 Recombina
Aay51880 Crosslink
                                                                                                                                                                                                                                   rropoelastin; hTB; elastin; glycosaminoglycan; GAG-binding; medical;
pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 253; DB 2; Length 216; 100.0%; Pred. No. 2.1e-17; ive 0; Mismatches 0; Indels C
                                                             ALIGNMENTS
                                                                                                                                                                                                              Human tropoelastin derivative SHEL26-36.
     ADE44977
AAY51880
                                                                                                                               AAY01310 standard; protein; 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 35; Page 11; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       97AU-00008117.
                                                                                                                                                                                                                                                                                                                                                                                              98WO-AU000564.
        ٦ ح
                                                                                                                                                                                       (first entry)
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        2257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 216 AA;
        58.9
                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                         WO9903886-A1
                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1997;
                                                                                                                                                                                       07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999
                                                                                                                                                                                                                                                                                                               Synthetic.
          149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weiss AS;
                                                                                                                                                             AAY01310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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AAW46315
                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                        RESULT 1
                                                                                                                       AAY01310
          99
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AAW46315 standard; protein; 730 AA.

AAW46315;

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This represents the human elastin sequence containing the minimal functional unit (MPU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has cont a naturally 5-7) amino acids and the MFU polypeptide may include at 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at can also be derived from the sequences of animal elastin, lamprin and can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides are self-aligning peptides capture used to coat prostheses made of animal or synthetic material or They are used to coat prostheses made of animal or synthetic material or comparable to the MFU as as blood vessel or heart valve replacements, metal, particularly for use as blood vessel or heart valve replacements.

Con high-tensile strength materials, e.g. ropes or parachute cord.

Cor high-tensile strength materials, e.g. ropes or parachute cord.

Cor high-tensile strength anterials, e.g. ropes or parachute cord.

Cor high-tensile strength materials, e.g. ropes or parachute cord.

Cor high-tensile strength materials, e.g. ropes or parachute and produce cordinate, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombosogenic and non-immunosperic than full-length elastins. They are non-thrombosomic and non-immunosperic properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. combining the properties to be tailored for particular applications, e.g. compared to the properties to be tailored for part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non-natural polypeptide with multiple beta-sheet, beta-turn
structures - particularly based on human elastin, useful for coating
prostheses, as wound dressings, etc., allows ingrowth of cells.
                                                                         MFU-1; minimal functional unit; elastin; human; fibrous protein;
beta-sheet; coating; wound dressing.
                              Human elastin containing non-natural polypeptide MFU-1 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 253; DB 2;
100.0%; Pred. No. 6.4e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                          374. .499
/note= "MFU-1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothstein SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEIN SPECIALTIES LID. (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY69068 standard; protein; 731 AA
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 1B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0023552P.
97US-00911364.
                                                                                                                                                                                                                                                                                                                                                                                    97WO-CA000560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keeley FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-145551/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothstein A,
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                               WO9805685-A2
                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                         12-FEB-1998
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                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY69068
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AAB66657;

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The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence specification describes tropoelastin derivatives, in which a subsequence of eliminated, or a subsequence has been inserted so that susceptibility to eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced elementary is an end an be used where the wild-type protein would be cusceptibility, and can be used where the wild-type protein would be cropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatived protease-susceptibility sites, are useful containing in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand conting in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand conting agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth containing conting the protease of cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by competases, or to limit protease activity that causes blood clotting ax
                                                                                                    Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 253; DB 3; Length 731; 100.0%; Pred. No. 6.4e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADBGVRR
                                                                   Amino acid sequence of a human tropoelastin splice form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 107-109; 136pp; English.
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          98AU-00004723.
                                                                                                                                                                                                                                                                                                                                                                                         99WO-AU000580.
                                  30-MAY-2000 (first entry)
                                                                                                                                                                                                                                441. .442
503. .504
515. .516
564. .565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-182399/16.
N-PSDB; AAZ61146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 731 AA;
                                                                                                                                                                                                                                                                                                                    WO200004043-A1
                                                                                                                                                                                                                              Cleavage-site
Cleavage-site
                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                     27-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell growth
 AAY69068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiss AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                             Homo
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Matches
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elastin polypeptide. This protein is useful in a cosmetic material or a prosthetic material such as prosthesis for blood vessel replacements, for heart valve replacement, tissue replacement, for covering burns, for
                                                                                                                                                                                                                                                                                                                              Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
                                                                                                                                                                                                                                                                                                                                                                                                                    of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; elastin; minimal functioning unit; MFU; prosthesis; bleta-sheev/beta-turn structure; fibrous protein; prosthesis; blood vessel replacement; heart replacement valve; burn; wound; lamprin; spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor; platelet activation inihibitor; non-thrombogenic; cell infiltration; non-immunogenic; blocompatible; high tensile strength; elasticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    unit (MFU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                           Minimal function unit; MFU; human; elastin prosthetic.
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a minimal functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 253; DB 4;
100.0%; Pred. No. 6.4e-17;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  Stahl R;
                                                   Human elastin protein without signal peptide.
                                                                                                                                                                                                                                                                              Keeley F, Rothstein S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU08725 standard; protein; 731 AA.
                                                                                                                                                                                                                                     (PROT-) PROTEIN SPECIALTIES LTD
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 39pp; English.
                                                                                                                                                                                                              99US-00340736.
                                                                                                                                                                                   29-JUN-2000; 2000WO-US017829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human elastin mature protein.
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                covering wounds and stents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                    (HSCR-) HSC RES & DEV LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                     WPI; 2001-102886/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 731 AA;
                                                                                                                                WO200100666-A2
                                                                                                         Homo sapiens
                                                                                                                                                                                                             29-JUN-1999;
                                                                                                                                                                                                                                                                             Rothstein A,
                           05-APR-2001
                                                                                                                                                          04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU08725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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99US-00340736.

29-JUN-1999;

03-DEC-2002.

Homo sapiens US6489446-B1

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Gaps

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49

AAB66657 standard; protein; 731 AA.

AAB66657

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Region

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Keeley F, Rothstein S;

HSC RES & DEV LP. PROTEIN SPECIALTIES LTD.

96US-0023522P. 97US-00911364.

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The invention describes a polypeptide (I) comprising a minimal functioning unit (MFU) which is present in the sequence of human elastin correctioning unit (MFU) which is present in the sequence of human elastin corrections are tructures, and at elast constitutions of a residue that participates in cross-linking, and not construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel control of the promote healing. MFUS can be co-aggregated with other proteins, for e.g. collagen, to provide prosthesis material that corresembles the natural structural materials of the body. MFUS modeled on resembles the natural structural materials of the body. MFUS modeled on resembles the natural structural materials of the body. MFUS modeled on a variety of materials, for a number of different applications, for e.g. in cords and ropes for use in parachutes and in cosmetics. Coating synthetic prosthesis with MFUS modeled on human elastin significantly synthetic prosthesis with MFUS modeled on human elastin significantly containing materials. In contrast correctioning is a single consultable fragments of elastin used before, an MFU is a single pertite of defined composition. The MFU is considerably smaller than the parent protein, simpler in structure, easier to produce or expression. Containing through the parent protein, simpler in structure, easier to produce or expression. The monopeal composed entirely of a human elastin sequence, MFU is non-thronded entirely of a human elastin sequence, MFU is non-thronded entirely of a human elastin sequence, mFU is non-immoral and entire and provides a friendly environment for cell infilation.
                                                                                                                                                                                                                                                      Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not naturally occurring fibrous protein.
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1B; 21pp; English
                                                                                                                                                                                                                    WPI; 2003-391056/37
                                                                                                                                                                        Rothstein A,
                       07-AUG-1996;
                                              07-AUG-1997;
                                                                                               (HSCR-)
                                                                                                                            (PROT-)
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ö immunogenic, thus providing a truly biocompatible material. MFUS modeled on lamprin and other fibrous proteins can be used to make a variety of materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human elastin on which the MFU peptides of the invention are based Gaps ; 1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR 49 Length 731; Indels unery Match 100.0%; Score 253; DB 6; Best Local Similarity 100.0%; Pred. No. 6.4e-17; Matches 49; Conservative 0; Mismatches n. Sequence 731 AA;

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fibrous protein; prosthesis; elastin; lamprin; spider silk protein; blood vessel; wound; burn healing; collagen. ADL96420 standard; protein; 731 Human elastin protein fragment (first entry) 20-MAY-2004 ADL96420; ADL96420 RESULT

Location/Qualifiers

Homo sapiens

Key

100.08; Conservative Similarity 49; Matches

This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, protein. The invention also describes a prosthesis control animal, or synthetic material comprising the polypeptide, an elastic material comprising the polypeptide, a high tensile strength material comprising the polypeptide, and the polypeptide comprising the or material comprising the or material comprising the or material comprising of a portion of the polypeptide comprising at least three beta sheet/beta turn portion of the polypeptide consisting essentially of a portion of the polypeptide consisting essentially of a portion of the polypeptide consisting essentially of a portion of an animal elast in comprising at least three beta sheet/beta turns, and (d) a cell amprin comprising at least three beta sheet/beta turns, and (d) a colypeptide consisting essentially of a spider silk protein comprising at least three beta sheets/beta turns, and (d) a cell amprin comprising at least three beta sheets/beta turns, a polypeptide having the primary structure of a portion of a naturally occurring three beta sheets/beta turns, a polypeptide is not a naturally occurring about 7 amino acids and the polypeptide is not a naturally occurring about 7 amino acids and the polypeptide is not a naturally occurring construct human elastin-like prostheses such as wound or burn bealing. Alternatively the MFU can be co-aggregated with other proteins, for example collagen, to provide prosthesis material that resembles the natural structural materials of the body. The MFU based material is such endothelial cells, and the prosthesis can become a permanent living containing materials is more biocompatible than other elastin . 0 Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns. Gaps ö 516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGRGAGPGFGADEGVRR 564 "region specifically claimed in claim 6" in claim 6" و. 49 Length 731; 607. .717 /note= "region specifically claimed in claim in claim 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR Indels /note= "region specifically claimed 188. .367 /note= "region specifically claimed 0; 100.0%; Score 253; DB 7; 100.0%; Pred. No. 6.4e-17; 0; Mismatches Rothstein S; Claim 5; Fig 1B; 17pp; English. 28-SEP-2001; 2001US-00964662 96US-0023522P 97US-00911364 99US-00340736 499 Keeley F, /note= 374. 45 (ROTH/) ROTHSTEIN A. WPI; 2003-898105/82. (KEEL/) KEELEY F. (ROTH/) ROTHSTEIN S. Sequence 731 AA; US2003166846-A1. Rothstein A, 07-AUG-1997; 29-JUN-1999; 07-AUG-1996; 04-SEP-2003 Query Match Best Local S Region Region Region g ð

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The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells contraining vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives for hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated sequence of the synthetic human tropoelastin SHEL
                                                                                                                                                                                                                        New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 253; DB 2;
ilarity 100.0%; Pred. No. 6.5e-17;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 82pp; English.
                   98WO-AU000564.
                                                        97AU-00008117.
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                                                                                         (UNSY ) UNIV SYDNEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li DY, Karnik S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 733 AA;
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                   17-JUL-1998;
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                                                                                                                                  Weiss AS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
the crosslinks. Such material may be useful in e.g. surgical
applications, where the gradual loss of material over time is intended.
(Updated on 25-MaR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic polynucleotide(s) - encode recombinant tropoelastins and
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                                                                                                                                                                                                          Tropoelastin; pharmaceutical; surgical dressing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 253; DB 2;
100.0%; Pred. No. 6.5e-17;
tive 0; Mismatches 0;
                                                                                                                                                                       Synthetic human tropoelastin (SHEL)
                                        AAR56653 standard; protein; 733 AA.
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                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 733 AA;
                                                                                                                                                                                                                                                                                    WO9414958-A1
                                                                                                                                                                                                                                                                                                                                                              16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1992;
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                                                                                                                 25-MAR-2003
22-MAR-1995
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                                                                             AAR56653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variants.
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Matches
     RESULT 7
                         AAR56653
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NAME OF COLORS O

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Gaps

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0; Indels

Length 733;

49

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Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
                                                                              Human; tropoelastin; elastin; body vessel occlusion; stenosis;
vascular smooth muscle cell; elastin signaling; vasctropic.
ABG75223 standard; protein; 757 AA.
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RESULT 8 AAY01301

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28-JAN-1999.

preventing stenosis

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(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
         Claim 24; Page 138-141; Opp; English.
                                                                                                                                                                                ADP65160 standard; protein; 757 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 56pp; English
                                                                                                                                                                                                                                                                                                        31-OCT-2001; 2001US-0336220P.
                                                                                                                                                                                                                                                                                              31-OCT-2002; 2002WO-US035433
                                                                                                                            Local Similarity 100.
nes 49; Conservative
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                                                                                                                                                                                                                                                                                                                                        WPI; 2003-712740/67.
                                                                                                                                                                                                                                                                                                                                             GENBANK; NP 000492.
                                                                                                            Sequence 757 AA;
                                                                                                                                                                                                                                                                         WO2003072827-A1.
                                                                                                                                                                                                                 Human elastin.
                                                                                                                                                                                                                                                     immune; human
                                                                                                                                                                                                                                                               Homo sapiens.
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(first entry)

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continuer compilers: a creatment or rneumatona arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; diagnosis or cefficacy of a candidate drug in vitro for the treatment of collagency of a candidate drug in vitro for the treatment of collagency induced arthritis, and reducing the symptoms associated with collagency arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antigout, antiinflammatory dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as the interval disease caused by an infectious agent. This sequence represents of immune disease caused by an infectious agent. This sequence represents of autoimmune diseases or arthritides. Note: This sequence represents of autoimmune diseases or arthritides. Note: This sequence is not shown of antoimmune diseases or arthritides. Note: This sequence is not shown or with the specification. It has been supplied in an electronic format from
The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of further comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tropoelastin derivative SHEL26-36 (excluding exon 26A product)
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100.0%; Pred. No. 6.7e-17;
iive 0; Mismatches 0;
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                                                                                                                             The present invention relates to the use of an agent that promotes clastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin obstruction, increasing F:G actin ratio in a smooth muscle cell; of polymerisation, increasing F:G actin ratio in a smooth muscle cell; of creating or preventing obstructive vascular disease (e.g. restenosis), or preventing stenosis. The agent that promotes elastin signaling in smooth muscle cells; decreasing vascular obstruction, promoting actin stress fiber formation or actin polymerization, increasing F:G actin ratio in a smooth muscle cell; treating or preventing obstructive actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis following analyplasty), or preventing treatment or preventing a medicament for the treatment or prevention of cclusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritis; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lugus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-products. The hybrid protein have controllable GAG-binding properties, products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHED26-36 excluding exon 26A product
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 183 AA;
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Gaps ., Length 183; 0; Indels 41 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA Pred. No. 1.9e-13; Score 212; DB 2; 100.0%; Preu. ... 83.8%; Query Match
Best Local Similarity
Local 41; Conservative à g

0

RESULT 12 AAY69138

AAY69138 standard; protein; 183 AA AAY69138;

30-MAY-2000 (first entry)

Amino acid sequence of a human tropoelastin derivative.

Tropoelastin, derivative, proteolysis; protease, antiwrinkle, hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage, elastin; cancer; metastasis; blood clotting.

Homo sapiens.

WO200004043-A1.

27-JAN-2000.

99WO-AU000580. 19-JUL-1999;

98AU-00004723 17-JUL-1998;

(UNSY) UNIV SYDNEY

Weiss AS;

WPI; 2000-182399/16

New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and growth

Disclosure; Page 134-135; 136pp; English.

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a increased. The derivatives have with reduced susceptibility, to proteolysis is used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide derivatives inhibition of protease activity. The tropoelastin derivative derivatives, and other polypeptides containing tropoelastin derivative. derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or

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growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration,
cell regeneration, membrane protein, signal transduction-related protein,
transcription-related protein, osteoporosis, neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide peptide of the polynucleotide by contacting the polynucleotide in an with the antibody of the encoded protein, and observing the binding expressible manner and an antisense polynucleotide. The oligonucleotide expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                   Length 183;
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                              41
                                                                                                                                                                                                                                                                                            AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41
                                                                                                                                                                                                                                                                    1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGFGA
                                                                                                                                                                                           83.8%; Score 212; DB 3; I
100.0%; Pred. No. 1.9e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein encoded by clone NT2RP70003110.
                                                                                                                                                                                                                                                                                                                                                                                                     ADB64761 standard; protein; 617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002EP-00007401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as targets of gene therapy.
                                                                                                                                                                                                                                 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J, Isono Y,
Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-450961/43.
                                                                                                                                                                                                               Similarity
                                                                                                                                                        Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADB62791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003
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                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                 Local
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Matches
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Sequence 660 AA;

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genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                      European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 617 AA;
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Gaps
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0
Length 617;
       Pred. No. 5.9e-13;
. wismatches 0; Indels
                                                41
                                      1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGA
 DB 7;
       100.0%; Preq. ...
  83.8%; Score 212;
                      Conservative
  Query Match
Best Local Similarity
                      41;
                       Matches
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RESULT 14 AAY01303

AAY01303 standard; protein; 660 AA AAY01303;

Human tropoelastin derivative SHELdeltamodified. (first entry) 07-JUN-1999

Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.

Homo sapiens. Synthetic.

WO9903886-A1

28-JAN-1999

98WO-AU000564. 17-JUL-1998; 97AU-00008117 18-JUL-1997;

(UNSY) UNIV SYDNEY

Weiss AS;

WPI; 1999-132162/11. N-PSDB; AAX27705

macromolecular binding properties, useful e.g. as surgical implants. New derivatives of human tropoelastin - with elastin-like or

Claim 7; Fig 3; 82pp; English

The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells contraining vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, planamaceutical, veterinary and cosmetic applications, e.g. as antiproducts. The hybrid protein have controllable GAG-binding properties, products. The hybrid protein have controllable GAG-binding properties, peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELdeltamodified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM05959-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                           ·.
Length 660;
                           Indels
                                                                                                                                                                                                                                                                             human; gene therapy; diagnostic marker; pharmaceutical.
                                                                          1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41
                              ö
                Pred. No. 6.3e-13;
 Score 212; DB 2;
                                                                                                                                                                                                                                               Human protein of the invention SEQ ID NO:2477.
            100.0%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2477; 305pp; English.
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Otsuka M,
                                                                                                                                                                ADM03792 standard; protein; 663
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    83.8%;
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                                   Conservative
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Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-723558/69.
      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                          20-MAY-2004
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                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T,
                                                                                                                                                                                               ADM03792;
                                   Matches
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41 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA g ò

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Gaps

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0; Indels

6.3e-13;

83.8%; Score 212; DB 7;

0; Mismatches

100.08;

41; Conservative

Matches

Query Match Best Local Similarity

Sequence 663 AA;

Length 663;

RESULT 16 ADE40134

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23-APR-2002;
                01-AUG-2002;
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ADE40134 standard; protein; 692 AA

ADE40134;

(first entry) 29-JAN-2004

Human NOV16b protein - SEQ ID 40.

NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antidatexinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV.

Homo sapiens,

WO2003064589-A2.

07-AUG-2003

02-AUG-2002;

2001US-0310951P. 2001US-0311292P. 2001US-0311979P. 2001US-0312892P. 2001US-0313201P. 16-AUG-2001; 13-AUG-2001; 03-AUG-2001; 07-AUG-2001;

2001US-0313702P. 2001US-0314031P. 2001US-0314466P. 2001US-0315403P. 2001US-0313415P. 2001US-0313643P. 17-AUG-2001; 20-AUG-2001; 21-AUG-2001; 23-AUG-2001; 20-AUG-2001;

2001US-0315853P. 2001US-0322716P. 2001US-0323994P. 2001US-0340233P. 28-AUG-2001; 29-AUG-2001; 17-SEP-2001; 21-SEP-2001; 14-DEC-2001;

2002US-0365478P. 2002US-0373814P. 2002US-0354591P. 2002US-0373825P. 2002US-0373989P 2002US-0374632P 05-FEB-2002; 19-MAR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002;

(CURA-) CURAGEN CORP.

2002US-0386971P 2002US-00210172 Miller CE, Patturajan M, Pena CEA, Rieger DK;
RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson I
Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
C JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR; Guo X, Zhong M, Gerlach V Edinger SR, Ellerman K, N Shimkets RA, Alsobrook J

Anderson DW;

WPI; 2003-663472/62. N-PSDB; ADE40133

or New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing pharmacogenomics.

Claim 1; SEQ ID NO 40; 560pp; English.

The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive,

Sequence 698 AA;

ö atherosclerosis, hypertension, cancer, obserty, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Albinimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may hybridiseation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention. The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins conteating the derivatives are useful in medical, planamaceutical, veterinary and cosmetic applications, e.g. as antiwirkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated human tropoelastin variant SHELdelta26A Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant. neuroprotective, nootropic, antiparkinsonian, antiasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, Gaps macromolecular binding properties, useful e.g. as surgical implants. immunosuppressive, anti-HIV, . 0 New derivatives of human tropoelastin - with elastin-like or Length 692; Indels 510 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 550 41 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA .. Score 212; DB 7; 1 Pred. No. 6.5e-13; 100.0%; Pred. No. o... Live 0; Mismatches Human tropoelastin variant SHELdelta26A. cytostatic, anorectic, antidiabetic, AAY01302 standard; protein; 698 AA. Claim 13; Fig 2; 82pp; English. 98WO-AU000564. 97AU-00008117. 83.8%; 07-JUN-1999 (first entry) 41; Conservative Local Similarity (UNSY) UNIV SYDNEY WPI; 1999-132162/11 Sequence 692 AA; sapiens WO9903886-A1 18-JUL-1997; 17-JUL-1998; 28-JAN-1999 Synthetic. Query Match AAY01302; Weiss AS; Matches RESULT 17 AAY01302 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ò A COURT OF C 6.6e-13;

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The present sequence represents a human reduced tropoelastin derivative, certificated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a consequence has been inserted so that susceptibility, to proteolysis is reduced or eliminated, or a consequence has been inserted so that susceptibility, or proteolysis is increased. The derivatives protein would be degraded too easily, e.g. in context with serum or wound exidate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative competitive inhibition of protease activity. The tropoelastin derivative derivation, particularly sites, are useful in human or veterinary derived protease-susceptibility sites, are useful in human or veterinary condition, particularly of smooth muscle cells, epithelial or growth inhibition, particularly of smooth muscle cells, epithelial or conductuatives are competitive inhibitores of the protease cleavage site in tropoelastin protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit controlling proteins blood clotting
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                                                                                                                                                                                                                                                                                                                                       Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
growth inhibition; peptidomimetic; lung damage; elastin; cancer;
                                        Gaps
                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human reduced tropoelastin derivative.
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0
     Length 698;
                                        Indels
                                                                                                 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41
       Score 212; DB 2; I Pred. No. 6.6e-13;
83.8%; bcc. No. c. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 110-112; 136pp; English.
                                                                                                                                                                                                      AAY69069 standard; protein; 698 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98AU-00004723.
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                                                                                                                                                                                                                                                                                                                                                                                                metastasis; blood clotting
                                                                                                                                                                                                                                                                              (first entry)
                                              41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNSY ) UNIV SYDNEY
            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                               Matches
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83.8%; Score 212; DB 3; Length 698;

Sequence 698 AA;

Query Match

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                                                                                                                                                                                                                     NOVX, cardiant, antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leiter MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
              Gaps
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              Indels
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                                   1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
100.0%; Prec. ...
                                                                                                                            ADE40132 standard; protein; 711 AA
                                                                                                                                                                                                   Human NOV16a protein - SEQ ID 38.
                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0309501P.
2001US-0310291P.
2001US-0310544P.
2001US-0310951P.
2001US-0311292P.
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2001US-0312892P.
2001US-0313201P.
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2001US-0314031P.
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2001US-0315403P.
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                                                                                                                                                                                                                                                                                                                                                                                                   2002WO-US024483
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                   tissue typing; human; NOV
      Local Similarity 100.
nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
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N-PSDB; ADE40131.
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17-AUG-2001;
20-AUG-2001;
20-AUG-2001;
21-AUG-2001;
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14-DEC-2001;
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17-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smithson G;
                                                                                                                                                                              29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
                                                                                                                                                      ADE40132;
        Best Loc
Matches
                                                                                                       RESULT 19
                                                                                                                    ADE40132
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                    Claim 1; SEQ ID NO 38; 560pp; English
                                    pharmacogenomics.
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypocensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.

Sequence 711 AA;

Score 212; DB 7; Length 711; 0; Indels 547 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 587 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41 100.0%; Pred. No. 6.7e-13; ive 0; Mismatches 0; 83.88; 41; Conservative Query Match Best Local Similarity Matches ð g

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Gaps

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RESULT 20 AAB08630

AAB08630 standard; peptide; 712 AA AAB08630;

(first entry) 20-DEC-2000

Amino acid sequence of a human elastin polypeptide.

Tropoelastin, elastin, elastic fibre, smooth muscle cell proliferation, smooth muscle cell differentiation, smooth muscle cell migration, smooth muscle cell function; atherosclerosis, restenosis, aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection, SVAS; hypertension; transplant arteriopathy.

Homo sapiens

WO200050068-A2

31-AUG-2000.

28-FEB-2000; 2000WO-US002526

26-FEB-1999;

(UTAH) UNIV UTAH RES FOUND.

Li DY; Keating MT, WPI; 2000-533134/48.

Blastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.

Example 3; Page 46; 79pp; English.

The present sequence represents a human elastin. Peptides derived from elastin are used in compositions of the invention. The specification

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describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprising: inhibiting the proliferation of smooth muscle cells in vivo; stimulating the migration of smooth muscle cell in vivo; and regulating the migration of smooth muscle cell in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a fusion protein, comprising human clastin and c-myc, preceded by a His tag. The protein is used in compositions of the invention. The specification describes elastin based proliferations that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based proliferations compositions compositions to a least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprising: inhibiting the proliferation of smooth muscle cells in vivo; stimulating the differentiation of smooth muscle cell in vivo; and regulating the
                                                                                                                                                                  by diminished capacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tropoelastin; elastin, elastic fibre, smooth muscle cell proliferation, smooth muscle cell differentiation; smooth muscle cell migration; smooth muscle cell function; atherosclerosis; restenosis, aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
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0
                                                                                                                                                                                                                                                                                                                         Length 712;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       548 AAAGLGAGIPGLGVGVPGLGVGAGVPGLGVGAGVPGFGA 588
                                                                                                                                                                                                                                                                                                                                                                                                    1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein comprising human elastin and c-myc.
                                                                                                                                                                                                                                                                                                                    83.8%; Score 212; DB 3; 1
100.0%; Pred. No. 6.7e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB08631 standard; peptide; 730 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 48; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000WO-US002526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00258217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                           41; Conservative
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li DY;
                                                                                                                                                                                                                                                                           Sequence 712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200050068-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08631;
                                                                                                                                                                                                                                                                                                                                                           Matches
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AAB08631
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Length 730;

83.8%; Score 212; DB 5;

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The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a control sample. A reduced level is indicative of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, aldehyda dehydrogenase 6, gravin, phospholipase C epsilon, elastin, insulin-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet derived growth factor receptor alpha, laminin M chain, subtilishin like protein PACE4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human elastin
migration of smooth muscle cells in vivo. The compositions may be used for the prophylaxis or treatment of a disorder characterized by diminished capacity to regulate smooth muscle cell function such as atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 monitoring of endometriosis, comprises detecting specific gene products, e.g. from the fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.
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                                                                                                                                                         DB 3; Length 730;
                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                            1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGA
                                                                                                                                              Score 212; DB 5, NO. 6.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kraetzschmar J,
                                                                                                                                                                           100.0%; Pred. No. 6.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 15-16; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                     AA017360 standard; protein; 730 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-2001; 2001EP-00250300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-01048633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haendler B,
                                                                                                                                                              83.88;
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro diagnosis and reduced expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hess-Stumpp H, Haend
Regidor P, Scotti S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-317413/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCHD ) SCHERING AG.
                                                                                                                                                                                 Local Similarity
                                                                                                                              Seguence 730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1191107-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                         AA017360;
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.
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Sequence 730 AA;

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                         Gaps
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                         0
                                                                                                                                                                                                                                                                     protein - SEQ ID 2566.
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                           Indels
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                                                                               1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                       1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 212; DB 8;
Pred. No. 6.9e-13;
          6.9e-13;
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        100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 2566; 210pp; English.
                                                                                                                                                                                                                                                                        Human soft tissue sarcoma-upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE08527 standard; protein; 870 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                          ADQ19747 standard; protein; 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2003; 2003WO-US038193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.8%;
                                                                                                                                                                                                                                             entry)
           Similarity 100.
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-441208/41.
                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 730 AA;
                                                                                                                                                                                                                                                                                                                                                                          WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                             26-AUG-2004
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Query Match
Best Local S:
Matches 41;
                                                                                                                                                                                                               AD019747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma.
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ID ADEC
                                                                                                                                               RESULT 23
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Homo sapiens. EP1067182-A2.

10-JAN-2001

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novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder.
                             Novel protein (useful for identifying genetic disorders) #682.
                                                                                                                                                                                                                   Goodrich RW, Ren F, Zhang
ehrman T, Weng G, Zhou P,
R, Xu C, Boyle BJ;
                                                                                                                                               2002US-0365091P.
2002US-0365384P.
2002US-0372381P.
                                                                                                                                 2001US-0339739P.
2001US-0339453P.
                                                                                                                 10-DEC-2002; 2002WO-US039555
                                                                                                                                                                      2002US-0372615P
2002US-00128558
                                                                                                                                                                                                             Asundi V, Goodric.
Xue AJ, Wehrman T
                                                                                                                                                                                      2002US-0376045P
               (first entry)
                                                                                                                                                                                                                                                  WPI; 2003-569235/53
                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                       N-PSDB; ADE07616
                                                                                                                                                                                                                                                                                                                                                                           the invention,
                                                                                  WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 870 AA;
                                                                                                                                                                                                                                  Wang D,
               29-JAN-2004
                                                                   Unidentified
                                                                                                                                                                      12-APR-2002;
22-APR-2002;
                                                                                                                                                                                     24-APR-2002;
                                                                                                                                                              L2-APR-2002;
                                                                                                                                               14-MAR-2002;
                                                                                                                                                       14-MAR-2002;
                                                                                                                                10-DEC-2001;
                                                                                                                                        11-DEC-2001;
                                                                                                 03-JUL-2003
ADE08527
                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                           Ghosh M,
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New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed. The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein Claim 20; SEQ ID NO 1593; 1177pp; English.

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Gaps
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0
        Length 870;
                              0; Indels
83.8%; Score 212; ...;
100.0%; Pred. No. 8.1e-13;
tive 0; Mismatches 0;
                           41; Conservative
              Similarity
  Query Match
Best Local S
             Best Loca
Matches
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1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGFGA 41

613 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGLGVGAGVPGFGA 653

AAB88422 standard; protein; 472 AA. AAB88422; RESULT 25 AAB88422

(first entry) 23-MAY-2001

Human membrane or secretory protein clone PSEC0191.

Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.

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which encode human secretory or membrane proteins represented by AAB88117

- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences of the
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The provention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used to suddy the expression and function of secretory
companies of used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
companies of expression and activity. The antibodies and antagonists
also be used as therapeutic agents to down regulate expression and
activity. The antibodies may also be used as diagnostic agents for
antagonists of expression and activity. The antibodies and antagonists
companies of expression and activity. The antibodies and antagonists
companies of expression and activity. The antibodies and antagonists
contivity. The antibodies may also be used as diagnostic agents for
activity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in samples (e.g. by enzyme
continue include rheumatoid arthritis and diabetes seases

very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.
                                                                                                                                                                                                                                                                                                                                                                             Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to nucleic acid sequences AAF93744
                                                                                                                                                                                                                                                                                                                                                                       Kawai Y, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T,
                                                                                                                                                                                                                   08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
                                                                                                                                                                   07-JUL-2000; 2000EP-00114090.
                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-093989/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF93849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 472 AA;
                                                                                                                                                                                                              08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                  Ota I,
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Wang J; Wang Z;

Zhao QA,

Zhang J, Zhao QA, ou P, Drmanac RT,

·. Score 208; DB 4; Length 472; Pred. No. 1.1e-12; 0; Mismatches 1; Indels Pred. No. 1.16 0; Mismatches 82.2%; 97.6%; Best Local Similarity 97.6 Matches 40; Conservative Query Match

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Gaps

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AAY69071 standard; protein; 571 AA. AAY69071;

RESULT 26 AAY6907

30-MAY-2000 (first entry)

Amino acid sequence of a human tropoelastin derivative.

Tropoelastin, derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting. inhibition;

98AU-00004723. 99WO-AU000580

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Disclosure; Page 115-117; 136pp; English.
                                                                                                                                                                                                                                                                                                               Rat Protein Q99372, SEQ ID NO 2524.
                                                                                                                                                                                                                                                                                  ADE56670 standard; protein; 864 AA
                                                                                                                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                                                                                                Best_Local Similarity 94.9
Matches 37; Conservative
                                                                        WPI; 2000-182399/16.
                                                     (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                  WO2003016475-A2.
                                                                                                                                                                                                                   Sequence 571 AA;
              WO200004043-A1.
                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003
     Homo sapiens.
                                            17-JUL-1998;
                                  19-JUL-1999;
                        27-JAN-2000
                                                                                        cell growth
                                                                                                                                                                                                                                                                                             ADE56670;
                                                                                                                                                                                                                             Query Match
                                                               Weiss AS;
                                                                                                                                                                                                                                                                         RESULT 27
                                                                                                                                                                                                                                                                               ADE5667
                                                                                                                                                                                                                                                                                        ð
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Score 189; DB 3; Pred. No. 1e-10; 0; Mismatches

74.78; 94.98;

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The invention discloses a composition comprising two or more isolated rat cor thuman polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a which is differentially expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polymptice sides given in the activity in an entend for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more confound that sequence presented is a rat protein (shown in Table 2 of the rappoint (CI) and spared nerve injury (SNI)) in an animal engagemental nerve injury (CMUMS), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal capmental or the sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed cor my more in which is differentially expressed during pain. Note: The sequence data for this patent did not form directly from WIPO at the my more than the correction or mane or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of chemotactic peptides which is incorporated into the surface
                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibroblast, elastic fibres; tissue regeneration; skin tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.5%; Score 181; DB 7; Length 864; 78.3%; Pred. No. 9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADBG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                    Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP71455 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                          Befort K,
                                                         14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 78.3
Matches 36; Conservative
                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a prosthetic device
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood vessel walls.
                                                                                                                                                                                                                                                          Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                              WPI; 2003-268312/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 864 AA;
                                                                                                                                                                                                                                                                                                                                          GENBANK; 099372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
09-JAN-2003
13-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP71455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP71455
           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be increased. The derivatives have with reduced susceptibility, and can be contact with serum or wound extdate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives of derivatives, and other polypeptides containing tropoelastin derivative. The derivative and commercias (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or competitive inhibition, particularly of smooth muscle cells, epithelial or competitive inhibitions of the protease cleavage site in tropoelastin editivatives are competitive inhibitions of the protease, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin controlling against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit propease activity that causes blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGCSGF 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGF 39
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1

Gaps

"N-terminal H or a biocompatible N-terminal group"

present up to 99 times"

a non-toxic metal

Ğ,

us-09-743-818a-72.rag

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The presence of the chemotactic peptide on the prosthetic device promotes invasion of the prosthesis by fibroblasts capable of synthesising elastic fibres, and so induces incorporation of the device into the regenerating natural tissue (esp.skin or blood vessel walls). The preferred devices contain 1 picomole-1 micromole nonamer (or repeating unit) per 100 square cm of surface, pref. incorporated by non-covalent bonding. (Updated on 099 -JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                       Prosthesis surface treated with chemo:tactic peptide - to induce invasion by fibroblasts and incorporation into regenerating tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein crystallisation, elastin, collagen, keratin, controlled release,
physical dimension, SELP9K gene monomer.
                                                /label= AGVPGFGV, AGVPGFG, AGVPGF, AGVPG, AGVP, AGV,

A or a covalent bond
                                                                                                                                                      /note= "C-terminal OH,OB3 where B3 is a nion, or a biocompatible C-terminal group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 GIPGLGVGVPGLGVGAGVPGLGVGAGVPGFG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SELP9K DNA gene monomer amino acid sequence.
                                                                          '', 'note= "N-cc.
e 18. 26
'*^= "may be absent, o
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Col 13-14; 12pp; English
                                                                      G, or a covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP53469 standard; protein; 60 AA.
                                                                                                                                                                                                                                                              85US-00793225.
                                                                                                                                                                                                                                        85US-00793225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.8%;
84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
                                                                                                                                                                                                                                                                                    (UYAL-) UNIV ALABAMA
                                                                                                                                                                                                                                                                                                                                  WPI; 1987-277253/39
                                                                                                                                                                                                                                                                                                             Long MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                           Misc-difference
                                                                                                                  Misc-difference
                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002045567-A1.
            Unidentified
                                                                                                                                                                                                                                      31-OCT-1985;
                                                                                                                                                                                                                                                             31-OCT-1985;
                                                                                                                                                                                        US4693718-A
                                                                                                                                                                                                             15-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002,
                                                                                                                                                                                                                                                                                                           Urry DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53469
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The present invention describes a composition (C1) comprising: (a) a protein polymer of at least 15kDa which comprises alternating blocks of at least 2 units each of a sequence of 3.30 amino acids which promotes protein crystallisation, and an amino acid sequence which is an elastinalise element, a collagen-like element or a keratin-like element; and (b) form under physiologically active substance. The composition acquires a non-liquid form under physiological conditions. Also described: (1) delivering a biologically active substance to a localized site in vivo, comprising administering C1, where the biologically active substance is delivered camensions of a body tissue of a mammal, comprising administering active composition is used for the controlled release of biologically active compounds in vivo. It can also be used to alter the physical dimensions of a body tissue. The present sequence represents a SELEPRY gene monomer harman alastic and active represents a SELEPRY gene monomer which are also as a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second or a second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elastin-like unit, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                 New composition comprising a repetitive polymer containing alternating blocks of sequences that promote protein crystallization and sequences that are elastin, collagen or keratin-like elements, useful for in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAGLGAGIPGLGV-GVGVPGLGV-----GAGVPGLGV-GAGVPGFGAGADEG
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%; Score 149; DB 5; Length 60; 61.1%; Pred. No. 1e-07; cive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 11; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR80339 standard; protein; 64 AA.
                         97US-00806029
                                                                       97US-00806029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAS SELP8K monomer sequence.
                                                                                                                                                                                                  ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US002728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                           Cappello J, Stedronsky
                                                                                                                   (CAPP/) CAPPELLO J. (STED/) STEDRONSKY E R.
                                                                                                                                                                                                                                              WPI; 2002-681318/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 33; Conser
                                                                                                                                                                                                                                                                     N-PSDB; ABQ82014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                              drug delivery.
                         24-FEB-1997;
                                                                     24-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09523611-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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3

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Gaps

0;

Length 34; Indels

Score 159; DB 1; Len Pred. No. 6.4e-09;

Pred. No. 6.4e 1; Mismatches

(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

03-MAR-1994;

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The sequence of the protein polymer adhesion substrate (PPAS) SELPBK monomer sequence. The gene sequence is altered from the native SELPB sequence (AAQ98718) by the introduction of a polymorphism at pos. 90 of the SELPB sequence. The sequence was used to produce the PPAS SELPBK (AAR80341). The protein can be used as a polymer substrate in a isopeptide cross-linking reaction catalysed by a transglutaninase enzymatic activity, e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material biological integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair
                                                                                                          Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.
                                                                                                                                                                                                        Example 7; Page 63; 138pp; English.
                                                            WPI; 1995-320413/41.
                                                                                N-PSDB; AAQ98722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64 AA;
                    Cappello J;
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3 Gaps 1 AAAGLGAGIPGLGV-GVGVPGLGV-----GAGVPGLGV-GAGVPGFGAGADEG 46 8 Query Match
Best Local Similarity 61.1%; Pred. No. 1.1e-07;
Matches 33; Conservative 5; Mismatches 8; Indels à

Search completed: November 19, 2004, 16:28:42 Job time : 10.014 secs

Alanine-c Protein p Protein p Polymer S Protein p Polymer S Protein p Protein p Protein p Amino aci EBSI mult EBSI mult EBSI mult EBSI synt EBSI Synt EBSI S

Aay31682 AAr80253 TAAr80252 EAr80252 EAr80251 AAr80254 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80255 EAr80256 EAr80255 EAr802556 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAr802552 EAR802552 EAR802552 EAR802552 EAR802552 EAR802552 EAR8025523 EAR802523 EAR8025523 EAR8

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AAR80255
ABP53476
AAW53519
AAP82957
AAR41008
                                                                                                                                                                                                                      AAW26343
AAY78278
ABG69268
ADE44969
                                                                                                                                                                                                                                                                                                AAW53544
AAY51888
ABG31418
ABW01634
ABP53478
ADK51953
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ABG69272
ADE44977
ADK51955
ABP53470
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AAW53523
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AAW49724
AAW09221
AAY51891
ABG31421
ABW01637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP53482
ABP53466
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ABP53481
AAW69213
AAW63541
AAW53541
AAW51897
AAW5189728
AAS18026
ABP53477
AAR92366
AAR41011
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FPGALVPGGVADAAAYKAAKACACLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL

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PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKKF

GAGAAGVI.PGVGGAGVPGVPGAI.PGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGIVPGG PGFGPGVVGVPGAGVPGAGIPVVPGAGIPGAAVPGVVSPBAAAAAAAKAAKYGAR

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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated tropoelastin derivatives of the invention a subsequence has been mutated or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be increased. The derivatives have with reduced susceptibility, and can be competitive inhibition of protease activity. The tropoelastin derivatives of erivatives, and other polypeptides containing tropoelastin derivative derivatives and other polypeptides containing tropoelastin derivative derived protease-susceptibility sites, are useful in human or veterinary derived protease-susceptibility sites, are useful in human or veterinary control of commetties (e.g. antiwrinkle or hand lotions), as bulking agents mud of the protease cleavage site in tropoelastin control of protecting state mimic the protease cleavage site in tropoelastin protecting against lung damage caused by elastin, for inhibiting or protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit
                                                                                                                                                                                                                                                                                                Tropoelastin; derivative; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
Aay31695 Fibronect
Aay80346 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2680; DB 3; Length 515; 100.0%; Pred. No. 5.4e-153;
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                                                                          ALIGNMENTS
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   AAY31695
AAY80346
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The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is
                                                                                                                                                                                                                                                                                             rropoelastin, derivative; proteolysis; protease; antiwrinkle;
hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
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                                                                     New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
              AKAAKYGYGTPAAAAKAAAKAAQFGLVPGYGYAPGYGVAPGYGVAPGYGLAPGYGYAPG
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                                                                                                       VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                               VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
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Homo

Synthetic.

WO9903886-A1

97AU-00008117. 98WO-AU000564

18-JUL-1997;

17-JUL-1998;

(UNSY) UNIV SYDNEY

WPI; 1999-132162/11.

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increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide derivatives, and other polypeptides containing tropoelastin derivatives. Competitive inhibition of protease activity. The tropoelastin derivatives of derived protease-susceptibility sites, are useful in human or veterinary and for inducing chemotaxis. They are also useful for proliferation or and for inducing chemotaxis. They are also useful for proliferation or commential cells, fibroblasts, osteocytes, chondrocytes and platelets. They protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, and are used for controlling localized growth of cancers or metastases, or to limit
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100.0%; Pred. No. 6e-153;
ive 0; Mismatches 0;
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                                                                                            Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL; variant.
                                                                                                                    VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLR 515
                                                                                                                                     Human tropoelastin variant SHELdelta26A.
                                                                                                                                                                                          AAY01302 standard; protein; 698 AA.
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100.0%; Score 2680; DB 2;
Best Local Similarity 100.0%; Pred. No. 7.1e-153;
Matches 515; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 2; 82pp; English.
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481 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR

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100.0%; Score 2680; DB 3;
100.0%; Pred. No. 7.1e-153;
ive 0; Mismatches 0;
                                                                                                                                                                                          Disclosure; Page 110-112; 136pp; English.
       AAY69069 standard; protein; 698 AA
                                                                                                                  99WO-AU000580.
                                                                                                                           98AU-00004723
                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 515; Conservative
                             (first entry)
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                                                                                              WO200004043-A1
                                                                              Synthetic.
Homo sapiens.
                                                                                                                   19-JUL-1999;
                                                                                                                              17-JUL-1998;
                                                                                                                                                                                   cell growth
                              30-MAY-2000
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                   AAY69069;
     AAY69069
RESULT
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WO9805685-A2
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07-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
                                                  Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease; antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition; peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
Amino acid sequence of a human reduced tropoelastin derivative.
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                       61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 120
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structures - particularly based on human elastin, useful for coating
prostheses, as wound dressings, etc., allows ingrowth of cells.
                                                                                                                         PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKF
                                                                                                                                                 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKK
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                                                                         PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAG1PGVGPFGGPQPGVPLGY
                                     1 GGVPGAIPGGVFGGVFYPGAGLGALGGGALGPGGKPLKFVFGGLAGAGLGAGLGAFPAVT
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Length 698; Indels

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functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide at can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides can also be apprides. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, or high-tensile strength materials, e.g. ropes or parachute cord. Prostheses based on the MFU allow penetration of endothelial cells, so become permanent, living, tissue replacements. The MFU polypeptides have better biccompatibility than Known elastin-based materials. They are well astinal home.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider
                                                                             This represents the human elastin sequence containing
                          Claim 5; Fig 1B; 39pp; English.
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Sequence 730 AA;

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                                                                            GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                              61 FPGALVPGGVADAAAAXKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                   PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
                                                                                                                                                                                                                       PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
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                                      0; Gaps
       100.0%; Score 2680; DB 2; Length 730; 100.0%; Pred. No. 7.4e-153; ative 0; Mismatches 0; Indels 0
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Query Match
Best Local Similarity 100.
Matches 515; Conservative
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AAY69068 standard; protein; 731 AA.

AAY69068 ID AAY6 XX RESULT

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The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be cascaptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The cropoelastin derivatives provide competitive inhibition of protease cativity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative drotease-susceptibility sites, are useful for tropoelastin derivatived protease-susceptibility sites, are useful containing tropoelastin derivatived proteins (e.g. antiwinkle or hand consection or growth inhibition, particularly of smooth cuseful for proliferation or growth inhibition, particularly of smooth contained site in tropoelastin derivatives are competitive inhibitors of chondrocytes and platelets. Peptidomimetics that mimic the protease conforting amage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting
                                                                                                           Tropoelastin, derivative, proteolysis, protease, antiwrinkle, hand lotion, bulking agent, chemotaxis, proliferation, growth inhibition, peptidomimetic, lung damage, elastin, cancer, metastasis, blood clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
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                                                                        Amino acid sequence of a human tropoelastin splice form.
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100.0%; Pred. No. 7.4e-153;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 107-109; 136pp; English.
                                                                                                                                                                                                                              Location/Qualifiers
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                                        (first entry)
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Matches 515; Conservative
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Cleavage-site
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                                      30-MAY-2000
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     AAY69068;
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                                                                                       PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAKAAAKF
                                                                                                                                                                                         PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
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                     1 GGVPGALPGGVPYPGAGGGALGGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic polynucleotide(s) - encode recombinant tropoelastins and variants.
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93AU-00009661
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(first entry)
   Conservative
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N-PSDB; AAQ70941.
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28-JUN-1993;
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22-MAR-1995
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     515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
                                                                                                                                                                                                               AKAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGLAPGVGTAPG
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                                                                                               GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKYGAAAGLVPGG
                                                                                                                 PGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKYGAR
                                                                                                                                                                                               PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                            PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF
                                                                Score 2680; DB 4; Length 731; Pred. No. 7.4e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unit; MFU; human; elastin prosthetic
                                                                                                                                                                                                                                                                                                                              515
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Best Local Similarity
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Disclosure; Page 30; 77pp; English.

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GAGAAGYI.PGYGGAGYPGYPGAI.PGI.GGIAGYGTPAAAAAAAAAAAAKAAKYGAAAGI.VPGG 300
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                    Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
the crosslinks. Such material may be useful in e.g. surgical
applications, where the gradual loss of material over time is intended.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                       1 GGVPGAIPGGVPYPGAGLGALGAGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVG
                                                                                                                                                                                                                             PGVYPGGVL.PGARFPGVGVL.PGVPTGAGVKPKAPGVGGAFAGIPGVQPFGGPQPGVPLGY
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                                                                                                                                                                                                                                                                                       421 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
                                                                                                      Length 733;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of synthetic human tropoelastin SHEL.
                                                                                                100.0%; Score 2680; DB 2;
100.0%; Pred. No. 7.4e-153;
ive 0; Mismatches 0;
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                                                                                                                  Matches 515; Conservative
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362

422 480 482

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0;
                                                                                                                                                                           The invention relates to a derivative or variant of human tropoelastin (INTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, products or absence of a specific fragment, designated sequence of the synthetic human tropoelastin SHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGALVPGGVADAAAAKKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAPAGIPGVGPFGGPQPPLGY
                                                                                                              New derivatives of human tropoelastin – with elastin-like or
macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 PGYYPGGVLPGARFPGVGVLPGVPTGAGYKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
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                                                                                                                                                      Disclosure, Fig 1; 82pp; English
    97AU-00008117
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 515; Conservative
                                                                           WPI; 1999-132162/11.
                          (UNSY ) UNIV SYDNEY
                                                                                       N-PSDB; AAX27704
                                                                                                                                                                                                                                                                                                                                                     Sequence 733 AA;
 18-JUL-1997;
                                                   Weiss AS;
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ABG75223 standard; protein;

RESULT 10 ABG75223 ID ABG7

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Hirsch R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the use of an agent that promotes elastin signaling in smooth muscle cells for decreasing or preventing occlusion of a body vessel by smooth muscle cells, decreasing vascular obstruction, promoting actin stress fiber formation or actin obstruction, increasing F:G actin ratio in a smooth muscle cell, preventing obstructive vascular disease (e.g. restenosis), or treating or preventing obstructive vascular disease (e.g. restenosis), muscle cells is useful for decreasing or preventing occlusion of a body wessel by smooth muscle cells, decreasing viscular obstruction, promoting vessel by smooth muscle cells, decreasing viscular obstruction, promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actin stress fiber formation, actin polymerization, increasing Fig actin stress fiber formation or actin polymerization, increasing Fig actin ratio in a smooth muscle cell, treating or preventing obstructive vascular disease (e.g. restenosis following angioplasty), or preventing stenosis. It is also useful in manufacturing a medicament for the treatment or prevention of occlusion of a vessel. The present sequence is the human tropoelastin protein as shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                   Use of an agent that promotes elastin signaling in smooth muscle cells for e.g. decreasing or preventing occlusion of a body vessel by smooth muscle cells, treating or preventing obstructive vascular disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                      Human; tropoelastin; elastin; body vessel occlusion; stenosis; vascular smooth muscle cell; elastin signaling; vasctropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2680; DB 7;
100.0%; Pred. No. 7.6e-153;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 138-141; Opp; English.
                                                                                                                                                                                                                                                                                         27-MAR-2002; 2002US-0368084P
                                                                                                                                                                                                                                                       27-MAR-2003; 2003WO-US009391
                                                                                                                                                                                                                                                                                                                         (UTAH ) UNIV UTAH RES FOUND
                                                                  Human tropoelastin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing stenosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 757 AA;
                                                                                                                                                                                                                                                                                                                                                               Karnik S;
                                                                                                                                                                                       WO2003082203-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515;
                                                                                                                                                         Homo sapiens
                                  12-FEB-2004
                                                                                                                                                                                                                          09-0CT-2003
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ABG75223;
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The invention relates to a novel method for diagnosing and analysing a autoimmune disease or arthritides. The method comprises obtaining a autoimmune disease or arthritides. The method comprises obtaining the mENA patient sample containing mENA, analysing gene expression using the mENA that results in a gene expression signature of the mENA, and using that egene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of or arthritides in the patient, where gene esignature. The invention of further comprises: a treatment of theumatoid arthritis; identification of further than a mouse; diagnosis of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; arthritide; gene expression analysis; rheumatic; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatoid arthritic; osteopathic; antigout; antinflammatory; dermatological; immunosmodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
                                                                                                                                                                                                                                                                                  AKAAKYGVGTPAAAAAKAAAKAAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVAPPG 480
                                                                                                                                                                                                                                        420
                                                                                                                                                                                                                                                                                                                                                                                                                                       447 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVGLAPGVAFG
                               gagaagyi,pgyggagypgypgai.pgiggiagygrpaaaaaaaaaakaakygaaagi,ypgg 326
                                                                                                                                                                          386
                                                                                                                                                                      pgrapovygvpgagypgagypgagipvvpgagipgaaypgayspeaaakaakkaakygar
                                                                                                                                                                                                                                        PGVGVGGIPTYGVGAGGFPGFGVGVGJIPGVAGVPSVGGVPGVGGVPGVGISFEAQAAAA
                                                                                                        PGFGPGVVGVVFGAGVPGVPGAGI PVVPGAGI PGAAVPGVVSPBAAAKAAAKAAKYGAR
VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USUAPGUGVAPGIGPGGVAAAAKSAAKVAAKAQLR 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page, 56pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP65160 standard; protein; 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2002; 2002WO-US035433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SL;
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efficacy of a candidate drug in vitro for the treatment of collagen-
induced arthritis, and reducing the symptoms associated with collagen-
induced arthritis. The compositions of the invention have the following
activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
methods and compositions of the present invention are useful for
rehons and compositions of the present invention are useful for
rheumatoid arthritis, lupus, anthylosing spondylitis, fibrositis,
fibromyalgis, osteoathritis, gout, juvenile rheumatoid arthritis, and an
immune disease caused by an infectious agent. This sequence represents a
protein sequence relating to the genes used in the analysis and treatment
of autoimmune diseases or arthritides. Note: This sequence is not shown
in the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGGL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                            100.0%; Score 2680; DB 7; Length 757; 100.0%; Pred. No. 7.6e-153; .ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                        Matches 515;
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fibrous protein; prosthesis; elastin; lamprin; spider silk protein; blood vessel; wound; burn healing; collagen.
                  ADL96420 standard; protein; 731 AA
                                                                              Human elastin protein fragment.
                                                             (first entry)
                                                            20-MAY-2004
                                                                                                                                 Homo sapiens
                                        ADL96420;
RESULT 12
          ADL96420
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1 GGVPGAIPGGVPYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT

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This invention describes a polypeptide that comprises three beta sheet/beta turn structures and that is not a naturally occurring fibrous protein. The invention also describes a prosthesis comprising an animal, polypeptide, a cosmetic material comprising the polypeptide, a negative polypeptide, an elastic comprising the polypeptide, an elastic comprising the polypeptide, and tensile strength material comprising the polypeptide of material comprising two or more comprising the polypeptide comprising two or more polypeptides selected from (a) a polypeptide consisting essentially of a portion of the polypeptide consisting essentially of a portion of the main acid sequence of an animal elastin comprising at least three beta sheet/beta turns, (c) a polypeptide consisting essentially of a portion of lamprin comprising at least three beta sheets/beta turns, a polypeptide having the primary collaboration of a naturally occurring fibrous protein and a structure of a portion of a naturally occurring fibrous protein and a secondary structure comprising at least three beta sheet/beta turns, secondary structure comprising at least three beta sheet/beta turns, creamed the polypeptide is not a naturally occurring fibrous protein and a where each of the beta sheet/beta turn structures comprises from its contains the protein comprising at least three beta sheet/beta turns, creamed the polypeptide is not a naturally occurring fibrous protein. The minimal functional unit (MTU) of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrous protein. The minimal functional unit (MFU) of the invention is useful to construct human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing. Alternatively the MFU can be co-aggregated with other proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for example collagen, to provide prosthesis material that resembles the natural structural materials of the body. The MFU based materials is subject to infiltration of cells growing in the patient, including endothelial cells, and the prosthesis can become a permanent living tissue replacement. The material is more blocompatible than other elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide for constructing human elastin-like prostheses such as tubes for blood vessel replacement and sheets for other uses such as wound or burn healing, comprises three beta sheets and three beta turns.
                                                                                  /note= "region specifically claimed in claim 6"
                                                                                                                                                                             <u>.</u>9
                                                                                                                                   in claim 6"
                                            /note= "region specifically claimed in claim
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0; Mismatches 1;
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        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Fig 1B; 17pp; English.
                                                                                                                                                                                                                                                                                    28-SEP-2001; 2001US-00964662.
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99US-00340736
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Matches 514; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (ROTH/) ROTHSTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-898105/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ROTH/) ROTHSTEIN S.
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                       Region
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Human; elastin; minimal functioning unit; MFU; prosthesis; beta-sheet/Deta-turn structure; fibrous protein; prosthesis; blood vessel replacement; heart replacement valve; burn; wound; lamprin; spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor; platelet activation inhibitor; non-thrombogenic; cell infiltration; non-immunogenic; blocompatible; high tensile strength; elasticity;
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                                                                                                                                                                                 PGFGPGVVGVPGAGVPGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGAR
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                                                                                                         FPGAL VPGGVADAAAA XKAAKAGAGI GGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
             PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
                                            PGVYPGGVLPGARRPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVFLGY
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SPECIALTIES LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human elastin mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                             ABU08725 standard; protein;
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07-AUG-1997;
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The invention describes a polypeptide (1) comprising a minimal comprised of at least three beta-sheet/beta-turn structures, and at and comprised of at least three beta-sheet/beta-turn structures, and at an east three beta-sheet/beta-turn structures, and not least one amino acid residue that participates in cross-linking, and not construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel construct human elastin-like prostheses such as tubes for blood vessel construct human elastin. The MFUS can be co-aggregated with other burns or wounds to promote healing. MFUS can be co-aggregated with other proteins, for e.g. collagen, to provide prosthesis material that compressed the natural structural materials of the body. MFUS modeled on resembles the natural structural materials of the body. MFUS modeled on resembles the natural structural materials of constructions, for e.g. a variety of materials, for a number of different applications, for e.g. collagen, with MFUS modeled on human elastin significantly contrast of more biocompatible than other elastin-containing materials. In contrast consubilised fragments of elastin need before, an MFU is a single consubilised fragments of elastin used before, an MFU is non-practical purposes Like other elastin preparations, the MFU is non-thromany composed entirely of a human elastin sequence, MFU is non-thromany composed entirely of a human elastin sequence, mFU is non-thromany composed entirely of a human elastin sequence, mFU is non-thromany composed entirely of a human elastin sequence, mFU is non-thromany composed entirely of a human elastin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogenic, thus providing a truly biocompatible material. MFUs modeled immunogenic, thus providing a truly biocompatible material. MFUs modeled on lamprin and other fibrous proteins can be used to make a variety of materials having high tensile strength, elasticity and plasticity of their parent proteins. This is the amino acid sequence of mature human elastin on which the MFU peptides of the invention are based
                            Claim 1; Fig 1B;
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9 1 GGVPGAIPGGVFYPPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT Gaps ; Length 731; Indels Score 2670; DB 6; Pred. No. 2.9e-152; 0; Mismatches 99.68; 99.6 Best Local Similarity 99.6 Matches 513; Conservative Sequence 731 AA;

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420 480 480 420 300 300 180 pgvgvggiptygydaggepgfgvgvggipgvagvpgvggvggvggvggvggvggybgvgispbagaaa akaakygygtpaaaaakaaakaaakaadegyypgygyapgygyapgygyapgygtapgygyapg PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKKAAAKF GAGAAGVLPGVGGAGVPGVPGALPGIGGIAGVGTPAAAAAAAAAAAAKYGAAAGLVPGG PGFGPGVVGVPGAGYPGVPGAGI PVVPGAGI PGAAVPGVVSPEAAAKAAAKYGAR PGVGVGGI PTYGVGAGGFPGFGVGVGGI PGVAGVPSVGGVPGVGGVPGVPGTSPEAQAAAA akaakygygtpaaaakaaakaaqpgijvpgygvapgygvapgygvapgygjapgyg PPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGI PGVGPFGGPQPGVPLGY GGVPGATPGGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 361 361 421 421 301 301 61 61 121 121 181 g à qq ð g ð g à g a δ

VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQIR 515

481

Novel polypeptide useful in prosthesis, has a secondary structure characterized by three beta-sheet/beta-turn structures, and is not naturally occurring fibrous protein.

481 VGVAÞGVGVAÞAIGÞGGVAÞAÞKSAAKVAĀKKOLR

us-09-743-818a-71.rag

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cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
                                                                                                                   antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; anorectic; attiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versus-host disease, Alabeimer's; Parkinson's; tissue typing; human; NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller CE, Patturajan M, Pena CEA, Rieger DK;
RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
hong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
R, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
-JP, Lepley DW, Burgess CE, Majumder K, Wolenc AR;
           ADE40132 standard; protein; 711 AA
                                                                                Human NOV16a protein - SEQ ID 38.
                                                                                                                                                                                                                                                                                                 2001US-0309501P.
2001US-0310291P.
2001US-0310544P.
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2001US-0311292P
2001US-0311294P
2001US-0313201P
2001US-0313415P
2001US-0313415P
2001US-0313402P
2001US-0313402P
2001US-0314466P
2001US-0314466P
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2001US-0323994P.
2001US-0340233P.
2002US-0354591P.
2002US-0365478P.
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2002US-0374632P.
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Voss EZ, buller Shong M, ueller St. Shong M, ueller St. Ellerman K, Malen Eller St. Eller DM, Bi
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20-AUG-2001;
21-AUG-2001;
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                                                          29-JAN-2004
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28-AUG-2001;
29-AUG-2001;
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                                   ADE40132;
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ADE40132
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The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antitarteriosclerotic, hypocensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, notropic, antiparkinsonian, antiasthmatic and preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may houtilised as vaccines whilst the nucleic acids may be used as hyperidisation probes, in gene therapy, chromosome mapping, tissue typing, the human NOV protein of the invention.
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aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
transmembrane receptor PTK7; collagen type XVIII alpha 1;
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                                                                                                                                                                                                                                                                     7; Length 711;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                               Score 2667.5; DB 7;
Pred. No. 4.1e-152;
0; Mismatches 0;
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                                                                                                                                                                                                                                                               . $5.66
                                                                                                                                                                                                                                                                           99.08;
                                                                                                                                                                                                                                                                        Local Similarity 99.0
les 515; Conservative
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                                                                                                                                                                                                                              Sequence 711 AA;
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, and a normal soft tissue sample from the samples and comparing the expression of the gene in both soft tissue samples, where a higher level expression of the gene in both soft tissue sample indicates the of protein expression in the first soft tissue sample indicates the cytostatic applications and may be useful for detecting soft tissue carcoma. The method of the invention has acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is that of a human soft tissue sarcoma-upregulated specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY 180
                                                                                                                                                                                                                                                                                                                                            soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                        Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGVPGAIPGGVPGGVFYPGAGLGALGGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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----GLVPGVGVAPGVGVAPGVGVAPGVGLAPG
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                                                                                                                                                                                                                                                                                                            Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
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                                                                           515
                                                                                              Query Match
Best Local Similarity 98.8%; Pred. No. 4.4e-152;
Matches 515; Conservative 0; Mismatches 0;
                                                                             475 VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 2566; 210pp; English.
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           421 AKAAKYGVGTPAAAAAAAAAAAAQF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                           ADQ19747 standard; protein; 730
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                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                        In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
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                      platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%; Score 2667; DB 5;
98.8%; Pred. No. 4.4e-152;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         Kraetzschmar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 15-16; 21pp; German.
                                                                                                                                                                                                   21-AUG-2001; 2001EP-00250300.
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                                                                                                                                                                                                                                                                                                                                 Scotti S;
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Best Local Similarity
Matches 515; Conserv
                                                                                                                                                                                                                                                                           (SCHD ) SCHERING AG
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                                                                                                                                   EP1191107-A2
                                                                                               Homo sapiens
                                                                                                                                                                       27-MAR-2002
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                                       PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
                                                             GAGAAGVI.PGVGGAGVPGVPGAI.PGI.GGIAGVGTPAAAAAAAAAAAKAAKXGAAAGI.VPGG
                                                                              PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPBAAAKAAAKAAR
                     PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
                                                                                                                                            PGVGVGGI PTYGVGAGGFPGFGVGVGGI PGVAGVPSVGGVPGVGGVPGVGI SPEAQAAA
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Amino acid sequence of a human elastin polypeptide. AAB08630 standard; peptide; 712 20-DEC-2000 AAB08630

Tropoelastin, elastin, elastic fibre, smooth muscle cell proliferation, smooth muscle cell differentiation, smooth muscle cell migration, smooth muscle cell migration, vascular bypass graft stenosis; transplant arteriopathy; dissection, SVAS; hypertension, transplant arteriopathy.

WO200050068-A2. Homo sapiens

31-AUG-2000

28-FEB-2000; 2000WO-US002526

99US-00258217 26-FEB-1999;

(UTAH) UNIV UTAH RES

Li DY; Keating MT,

WPI; 2000-533134/48

Vascular bypass graft stenosis, transplant arteriopathy, ssection SVAS and/or hypertension. based compositions useful for treating atherosclerosis, restenosis, vascular aneurysm, dissection Elastin

Example 3; Page 46; 79pp; English.

The present sequence represents a human elastin. Peptides derived from elastin are used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth muscle cell proliferation, differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins (or fragments of them) which have biological activities comprising: inhibiting the proliferation of smooth muscle cells in vivo;

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imulating the differentiation of smooth muscle cell in vivo; and gulating the migration of smooth muscle cells in vivo. The compositions Y be used for the prophylaxis or treatment of a disorder characterized diminished capacity to regulate smooth muscle cell function such as
                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                             146
                                                    atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm and/or dissection. Disorders which may be treated also include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                     206
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                                                                                                                                                                                                                    Tropoelastin, elastin, elastic fibre, smooth muscle cell proliferation, smooth muscle cell differentiation; smooth muscle cell migration, smooth muscle cell function; atherosclerosis, restenosis, aneurysm; vascular bypass graft stenosis; transplant arteriopathy; dissection; SVAS; hypertension; transplant arteriopathy.
                                                                                                                                                                                               1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                      FPGALVPGGVADAAAAXKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
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                                                                                                                                                  Length 712;
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                                                                                                                                              Score 2663; DB 3;
Pred. No. 7.5e-152;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein comprising human elastin and c-myc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB08631 standard; peptide; 730
                                                                                                                                              99.4%;
                                                                                                                                                     Local Similarity conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                               Sequence 712 AA;
  stimulating
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                                                                                                                                        Query Match
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Matches
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8.86666666888
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                               NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic; antidabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; antitiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK; Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ; Voss EZ, Boldog FL, Gorman L, Leite MM, Vernet CAM, Anderson DW; Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Syytek KA; Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ; Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
                       516 VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 556
ADE40134 standard; protein; 692 AA
                                                                                                                                                                                                                                                      Human NOV16b protein - SEQ ID 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-Aug-2001; 2001us-0310951F.

09-Aug-2001; 2001us-0310951F.

09-Aug-2001; 2001us-0311292P.

15-Aug-2001; 2001us-0313201P.

17-Aug-2001; 2001us-0313201P.

17-Aug-2001; 2001us-0313415P.

20-Aug-2001; 2001us-0313415P.

21-Aug-2001; 2001us-0313445P.

21-Aug-2001; 2001us-0314466P.

28-Aug-2001; 2001us-0314466P.

29-Aug-2001; 2001us-0315458P.

29-Aug-2001; 2001us-0315458P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-2001; 2001US-0322716P.
21-SEP-2001; 2001US-0323994P.
14-DEC-2001; 2001US-0340233P.
05-FEB-2002; 2002US-0354591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-2002; 2002US-0365478P.
19-APR-2002; 2002US-0373814P.
19-APR-2002; 2002US-0373825P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-2002; 2002US-0373989P.
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2002US-0386971P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0310291P.
2001US-0310544P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2002; 2002WO-US024483
                                                                                                                                                                                                                    29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-663472/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADE40133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edinger SR, El.
Alsobrook JP, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003064589-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003
                                                                                                                                                                                  ADE40134;
                                                                                                    RESULT 19
                                                                                                                         ADE40134
                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a fusion protein, comprising human classin and c-myc, preceded by a His tag. The protein is used in compositions of the invention. The specification describes elastin based compositions that are potent regulators of smooth wuscle cell compositions that are potent regulators of smooth wuscle cell compositions differentiation and migration in vivo. The elastin-based compositions comprise at least one elastic fibre, elastins, tropoelastins compositions comprise at least one elastic fibre, elastins, tropoelastins compositions composition of smooth may biological activities comprising; inhibiting the proliferation of smooth muscle cells in vivo; and regulating the che differentiation of smooth muscle cell in vivo; and regulating the migration of smooth muscle cell in vivo; and regulating the for the prophylaxis or treatment of a disorder characterized by for the prophylaxis or treatment of a disorder characterized by atherosclerosis, restenosis, vascular bypass graft stenosis, transplant atteriopathy, aneurysm and/or dissection. Disorders which may be treated are include SVAS (undefined), hypertension, and transplant arteriopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGVGVGGIPTYGVGAGGFPGFGVGVGGTPGVAGVPGVGGVPGVGGVPGVGGVPGVGTSPEAQAAAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKAAKYGVGTPAAAAKAAAKAAAQF-----GLVPGVGVAPGVGVAPGVGVAPGVGLAPG 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPGALVPGGVADDAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGVPGAIPGGVPYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                    Elastin based compositions useful for treating atherosclerosis, restenosis, vascular bypass graft stenosis, transplant arteriopathy, aneurysm, dissection SVAS and/or hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 2663; DB 3; Length 730; 98.7%; Pred. No. 7.7e-152; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 48; 79pp; English.
                                                                               28-FEB-2000; 2000WO-US002526
                                                                                                                       99US-00258217
                                                                                                                                                               (UTAH ) UNIV UTAH RES FOUND
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Matches 514; Conserv
                                                                                                                                                                                                                                             WPI; 2000-533134/48.
                                                                                                                                                                                                         Keating MT, Li DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 730 AA;
                                                                                                                            26-FEB-1999;
                                            31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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PTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGV 428
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                                                                                                               2001US-0339739P.
2001US-0339453P.
2002US-036501P.
2002US-0365384P.
2002US-0372381P.
2002US-0372381P.
                                                                                         10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                          24-APR-2002; 2002US-0376045P
                                                                                                                                                                                                                                   Asundi V, Goodric
Xue AJ, Wehrman T
ang D, Chen R, Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462; Conservative
                                                                                                                                                                                                                                                                                WPI; 2003-569235/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                             WO2003054152-A2
                                                                                                                                                                                                                                                                                             N-PSDB; ADE07616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 870 AA;
                                                                                                                                                                                                                                                              Wang D,
                        Unidentified
                                                                                                                                      14-MAR-2002;
                                                                                                                                              14-MAR-2002;
12-APR-2002;
                                                                                                                                                                     12-APR-2002;
22-APR-2002;
                                                                                                                         11-DEC-2001;
                                                                                                                                                                                                                                    Tang YT,
                                                                                                                                                                                                                                                 Ghosh M,
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                                        The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiaschmatic and gynaecological activities and may be useful in diagnosing, treating or atherosclerosis, hyperternsion, cancer, obesity, diabetes, AIDS, multiple atherosclerosis, graft-versus-host disease, allabeimer's disease, Parkinson's be utilised as vaccines whilst the nucleic acids may be used as bybridisation probes, in gene therapy, chromosome mapping, tissue typing, the human NOV protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 AKAAKYGVGTPAAAAAKAAAKAAQFALINIAGIVPGVGVAPGVGVAPGVGVAPGVGVAFGYGVAFG
                                                                                                                                                                                                                                                                                   FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
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                                                                                                                                                                                                                                                                                                                                                           121 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGYGGAFAGIPGVGPFGGPQPGVPLGY
                                                                                                                                                                                                                                                                                                                                                                                   -----PGVGGAFAGIPGVGPFGGPQPGVPLGY
                                                                                                                                                                                                                                                                    GGVPGAIPGGVFGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAAGVLPGVGGAGVPGVPGVPG1PGIGGIAGVGTPAAAAAAAAAAAKAAKXGAAAGLVPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGGVFGVGISPEAQAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (useful for identifying genetic disorders) #682.
                                                                                                                                                                                                                                 Length 692;
                                                                                                                                                                                                                                                      Indels
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Pred. No. 5.9e-138;
                                                                                                                                                                                                                                                 0; Mismatches
                    Claim 1; SEQ ID NO 40; 560pp; English.
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                                                                                                                                                                                                                           90.78;
                                                                                                                                                                                                                                             Matches 477; Conservative
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                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                    Sequence 692 AA;
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                        New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                              Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 GAGEGALGGGALGPGGKPLKPDARILGAFGAVPGGLAGAGLGAGLGAFPAVTFPGALVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGLGALGGGALGPGKPLKP------VPGGLAGAGLGAGLGAFPAVTFPGALVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GVADAAAAYKAAKA-----GVGLPGVYPGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L.PGARFPGVGVL.PGVPTGAGVKPKAPGVGGAFAG1.PGVGPFGGPQPGVPLGYP1KAPKL.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 LPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAKAAAKFGAGAAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 GGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAAKAAAKFGAGAAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGFGFGPGVV
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                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                        J, Zhao QA,
Drmanac RT,
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                  Zhang
Goodrich RW, Ren F, Zhang
ehrman T. Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 2353; DB 7;
91.1%; Pred. No. 3.4e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                             Weng G, Zl
Boyle BJ;
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                                                   an T,
Xu C,
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199 128

285 248

379

416

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AAAAAKAAYYGYGTPAAAAAKAAAKAAQFGLVPGYGYAPGYGYAPGYGYAPGYGYAFGYGTAPGYG 476
                                                                                                                                                                                                                                                                                    PGGPGFGPGVVGVPGAG-VPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAK 356
                                                                                                  FGAGAA--GVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAAKAAKYGAAAGIV
                                                                                                                                             200 FGAGAAGFGAVPGVGGAGVPGAFGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLV
                                                                                                                                                                                               260 PGGPGFGPGVVVGVPGFGAVPGVVPGAGIPVVPGAGIPGABGFGAVSPEAAAKAAAKAAAK
                                                                                                                                                                                                                         YGARPGVGVGGI PTYGVGAGAFPGFGVGVGGI PGVAGVPSVGGVPGVGGVPGVGTSPEAQ
                                                                                                                                                                                                                                       180 YPIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAA
PGVYPG-GVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGFPQPGVPLG
                                                                                                                                                                                                                                                                                                                      477 VAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
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                                                                                                                                                                                                                                                                                                                                                                                                           ADM03792 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Sugiyama T,
J, Isono Y, H
Yoshikawa T, O
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N-PSDB; ADM01349.
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Yamamoto J,
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                                                                                                                                          240 ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are comprising the nucleic acids encoding the variants or derivatives are bybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHELdeltamodified
                                                  GTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVG 488
                                                               1 GGVPGALPGGVPRYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                         Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical; pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food; hand lotion; surgical implant; industrial product; human; SHEL.
              New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.9%; Score 2328; DB 2;
89.0%; Pred. No. 8.4e-132;
iive 3; Mismatches 8;
                                                                                                                                                                                                                                                      Human tropoelastin derivative SHELdeltamodified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGVPGAVPGGVPGGVFYPGAGFGA-----
                                                                                                                           VAPGIGPGGVAAAKSAAKVAAKAQLR 612
                                                                                                       VAPGIGPGGVAAAAKSAAKVAAKAQLR
                                                                                                                                                                                      AAY01303 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 3; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   97AU-00008117.
                                                                                                                                                                                                                                                                                                                                                                                                              98WO-AU000564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462; Conservative
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-132162/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNSY ) UNIV SYDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 660 AA;
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                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                   WO9903886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1997;
                                                                                                                                                                                                                                      07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1999
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Best Local S:
Matches 462
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                                                                                                                                                                                                               AAY01303;
                                                                                                          489
                                                             429
                                      994
                                                                                                                                                                   RESULT 21
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, Sato H, Ishii S;
i K, Irie R, Tamechika I;
Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                   human; gene therapy; diagnostic marker; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuki T, Wakamatsu A,
Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, M
Human protein of the invention SEQ ID NO:2477
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or

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                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAAGYIPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKXGAAAGIVPGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAKKAAKKGAR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 PGVGVGGIPIYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVGGVPGVGGVPGVGGVPBAAAA 415
            useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
      The polynucleotides ADM01316-ADM03758 are
                                                                                                                                                                                                                                                      61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                                                                                                                  -----AGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                             GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                121 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGGPGPGVPLGY
                                                                                                                                                                                                                                                                                                                                             116 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
                                                                                                                                                                                                                                                                                                                                                                           181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKF
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                                                                                                                                                                         61;
                                                                                                                                                                                                                    Length 663;
                                                                                                                                                                       Indels
                                                                                                                                        DB 7;
                                                                                                                                                                          5.
                                                                                                                                        Score 2306.5; DB 7
Pred. No. 1.6e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 AKAAKYGVGTPAAAAAKAAAKAAQFGLV-
   detecting the polynucleotide.
                                                                                                                                          86.1%;
                                                                                                                                                Best Local Similarity 87.8%;
Matches 452; Conservative
                                                                                                      Sequence 663 AA;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                      77
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446 VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLR 480
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180

162 240 222

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283

120 136

Human protein encoded by clone NT2RP70003110. 617 ADB64761 standard; protein; (first entry) 04-DEC-2003 ADB64761

Human, pharmaceutical, diagnostic, gene therapy; tissue regeneration, cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein, osteoporosis, neurological disease;

Homo sapiens

EP1308459-A2

28-MAR-2002; 2002EP-00007401.

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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel comparison to the polynucleotide, an antibody binding to the polynucleotide or its partial peptide, immunologically assaying the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of with the antibody of the encoded protein, and observing the binding expressible manner and an antisense polynucleotide. The oligonucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide of detecting the polyvucleotide. The polynucleotide or as a probe of the encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related of genes may be included in them, for developing a diagnostic marker or of gene therapy. The genes are involved in tissue and activity, or as targets respendence for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and, or cell transcription-related proteins, signal transduction-related proteins, diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded proteins and sequence data for this patent is not represented in the printed burnar nature of the protein of the invention. Note: Some of the privated privation is patent is not represented in the printed burnar nature.
                                                                                                                                               Irie R, Tamechika I;
                                                                                                                                                                                                                                                              a diagnostic
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                                                                                                                                                                                                                                               New polynuclectides and polypeptides, useful for developing a diagnos marker or medicines for regulation of their expression and activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGVPGAIPGGVFGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GGVPGAIPGGVPGGVFYP------ALGPCGKPLKPVPGGLAGAGLGAGLGAFPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGVYPGGVLPGARFFBGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 PGVYPGGVL-----PGVGPFGGPQPGVPLGY
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                                                                                                                             Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89;
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                                                                                                                           Sato H,
                                                                                                                                         Otsuka K, Nagai K, Irie
4, Nagahari K, Masuho Y;
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                                                                                                                     Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2129.5; DB 7
Pred. No. 6.2e-120;
0; Mismatches 1;
                                                                                                                                     Hio Y, Otsu
Otsuka M, 1
                                                                                                                     Otsuki T,
                                                        (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 222pp; English.
                     25-JAN-2002; 2002US-00350978
   05-NOV-2001; 2001JP-00379298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.5%;
82.5%;
                                                                                                                                                                                                                                                                                      as targets of gene therapy
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                                                                                                               Isogai T, Sugiyama T,
Yamamoto J, Isono Y, ]
Seki N, Yoshikawa T,
                                                                                                                                                                                          2003-450961/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 425; Conserv
                                                                                                                                                                                                             N-PSDB; ADB62791
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                                                                                                                                                      Seki N,
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The invention discloses a composition comprising two or more isolated rat cor human polymucleotides or a polymucleotide which represents a fragment, or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence comprising the vector identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a corporate of that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates subjected to pain, a method for producing is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a polymucleotides equence which is differentially compound that regulates the activity of one or more of the composition, a pecification, a method for producing a pharmaceutical composition, a cutivity in an animal of one or more of the polypeptides of identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides or method for identifying a compound that composition comprising the one or more pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for prepazing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                  480
                                                                                                                ----GLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG 417
                                         ----EAQAAAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
361 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA
                                                                               akaakygygtpaaaaakaaakaaqpgijvpgygyapgygyapgygyapgyglapgygyapg
                                                                                                                                                               VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 515
                                                                                                                                                                                                    vgvapgvgvapgigpggvaaaksaakvaakaouk 452
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                                               pgvgvggipiygvgaggepgegvgvga----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                           ADES6670 standard; protein; 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein Q99372,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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428 VGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGV 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 GVPGVGVPG------AGIPVVPGAGIPGAAV---PGVVSPEAAAKAAKKA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 GIPGVGIPGVGGIPGVGGIPGVGGPPGVGGPGIGGPGIVGGPGAVSPAAAKAAKAAKY 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 GARGGV---GIPTYGVGAGGFPGYGYGAGAGLGGASQAAAAAAAAAAKKGAGGAGTLGG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 AGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAKAAKYGAAAGLVPGGPGPGPGVGVPGA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 gdirdgadalipdigdirdadirbaaakaakaakkydaagdivrdgrd----vrvrda 376
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                                                                                                                                                                                               49
                                                                                                                                                                                                                           89
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                   ĠAĠĹSY--ASRPGĠVĹVPĠĠCĀGĀĀĀĀŶKĀĀĀKĀĠĀĠĹĠĠſĠĠVPGGVGVGGVPGAVGVG
                                                                                                                                                                                                                                                                                                                --GGLGVSAGAVVPQPGAGV----KPGKVPGVGLPGVYPGGVLP--GARF
                                                                                                                                                                                                                                                                                                                                   148 GVPGAVGGIGGLGVSTGAVVPQLGAGVGAGGKPGKVPGVGTPGVPGGVLPGTGARF
                                                                                                                                                                                                                                                                                                                                                                           PGVGVLPGVPTGAGYKPKAP-GVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGL
                                                                                                                                                                                                                                                                                                                                                                                                  pgvgvLbgvPrdrgvkakvPgdgggaFsGIPGvGPFGGQQPgVPLGYPIKAPKLPGGYGL
                                                                                                                                                                                                                          30 GGVPGGLPGGVPGGVXYPGAGIGGGLGGGALGPGGKPPKPGAGLLGAFGAGPGGAGA
                                                                                                                                                                   Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 864;
                                                                                                                                                                                                                                                          GAGLGAFPAVTFFGALVPGGVADAAAAYK-AAKAGAGLGGVPGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human membrane or secretory protein clone PSEC0191.
                                                                                                                                           DB 7;
                                                                                                                                                                                                  GGVPGAIPGGVPYPGAGL-GALGGGALGPGGKPLKP
                                                                                                                                     62.5%; Score 1675.5; DB 7; 60.9%; Pred. No. 1.3e-92; or. Mismatches 78;
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                                                                                                                                                                        17; Mismatches
                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                               Similarity
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                                                                                                                   Sequence 864 AA;
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Best Local Simi
Matches 383;
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                                                      Nishikawa T,
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
                 07-JUL-2000; 2000EP-00114090
                                                                                                                                                                                                                            Matches 284; Conservative
                                            (HELI-) HELIX RES INST
                                                             WPI; 2001-093989/11.
                                                     Ota T, Isogai T,
                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                  N-PSDB; AAF93849
                                                                                                                                                                                                            Sequence 472 AA;
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                          08-JUL-1999;
        10-JAN-2001
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à g à 엄 8 g This invention relates to nucleic acid sequences AAF93744 - AAF93916

which encode human secretory or membrane proteins represented by AAB88317

- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and

AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the

invention. The invention also includes methods for the production of

antibodies directed against the proteins, and cDNA sequences of the

antibodies directed against the proteins, and cDNA sequences. Which can

therapy. The polynucleotide sequences can be used in gene

therapy. The polynucleotide sequences and the proteins they encode may be

cused in the prevention, treatment and diagnosis of diseases associated

with inappropriate secretory protein/membrane protein expression. The

nucleic acids and complementary sequences may also be used as DNA probes

in diagnostic assays (e.g. polymerase chain reactions (PCR) to detect

and quantitate the presence of similar nucleic acid sequences in samples.

Chey may also be used to study the expression and function of secretory

proteins/membrane polypeptides and their role in metabolism. The

proteins/membrane polypeptides and their role in metabolism. 5 120 9 87 polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as agines for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes 81 acids encoding secretory proteins/membrane proteins, useful in 1 GGVPGAIPGGVFGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVT 27 GGVPGAIPGGVPGGVPYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGA----61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGL 2; Indels 226; Gaps Hayashi K; gene therapy or as candidate target molecules in drug development 49.0%; Score 1314; DB 4; Length 472; 55.1%; Pred. No. 3.7e-71; Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English. Kawai Y, Sugiyama T, -----TGGAGI--

181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGYGPQAAAAAAAAKF 240 241 GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAAKAAKYGAAAGLVPGG 300 ----AAAAAAAAKAAKYGAAAGLVPGG 119 301 PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVFGVVSPEAARAAKAAKYGAR 360 121 PGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGY -----PGGVVGA------GP

40;

Indels 115; Gaps

Length 745;

34.0%; Score 911.5; DB 2; 44.8%; Pred. No. 7.2e-47; Live 30; Mismatches 182;

Conservative

Query Match Best Local Similarity Matches 265; Conserv

Sequence 745 AA;

420 120 PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGAR 179 180 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVGGVPGVGGVPGVGGSPEAQAAAA 239 -----GLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG 280 The present sequence represents novel alanine-containing polymer IV that augmentation by injecting a polymer comprising repeating petitie monomeric units selected from nonapetide, pentapeptide and tetrapeptide monomeric units selected from nonapetide, pentapeptide and tetrapeptide monomeric units selected from nonapetide, pentapeptide and tetrapeptide separated by dynamic bridging segments. The polymer has an inverse temperature, and is injected in water solution at coacervate concentration. The polymer is injected at periurehral or subdermal sites (for treatment of urinary incontinence or for cosmetic purposes), or into application is restoration of intervertebral discs. Polymer IV has a Tt value of 28 deg AMUSMENTATION OF restoration of mammalian tissue by injecting solution of peptide polymer, used for soft or hard tissue reconstruction, especially of intervertebral disks. 361 PGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAA 421 AKAAKYGVGTPAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG Elastomer; bioelastomer; polymer IV; tissue augmentation; tissue restoration; tissue reconstruction; tissue repair; implant; fibronectin cell attachment site. 481 VGVAPGVGVAPGIGPGGVAAAKSAAKVAAKAQLR 515 281 VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLR 315 Alanine-containing elastomer, polymer IV. Claim 73; Page 106-109; 133pp; English. AAY31682 standard; protein; 745 Augmentation or restoration of Glazer 99WO-US004440 98US-0087155P (BIOE-) BIOELASTICS RES LTD. (first entry) 240 AKAAKY-----Urry DW, Parker TM, WPI; 1999-540487/45. 22-NOV-1999 26-FEB-1999; WO9943271-A1 27-FEB-1998; 29-MAY-1998; 02-SEP-1999 Synthetic. AAY31682; RESULT 26 AAY31682 ID AAY3 XX

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-GIPTYGVGAGGFPGFGV-GVG----GIPGV----AGVP 395
                                                                                                                                                                                                                                                                                                                                                              SVG----GVPGVG-----GVPGVGISPBAQAAAAKAAKY-GVGTPAAAAAKAAAKAAQFG 446
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                                                                                                                                                 GYPGYGYPGYGYPGYGYPGYGYPGYGYPGYGYP-----GYGYPGYPGYPGYGY 350
                                                                                        GVKPG-KVPGVGLPGV-YPGGVLPGARFPGVGV----LPGVPT-GAGVKPKAPGVGGAFA 161
                                                                                                            LGAFPAVTFPGALVPG-GVADAAAAYKAAKAGAGLGGVPGVG---GLGVSAGAVVPQPGA 108
                                                                                                                                                                                                                                                                                                                                                                                   AGKAGYPTGTGVGPQAAAAAAAAKAAAKFG-AGAAGVLPGVG---GAGVP--GVPG-AIPG
                                                                                                                                                                                                                            IG----GIAGVGTPAAAAAAAAKAAKYGAAAGLVP--GGPGFG-PGV----VGVPPGAG
                                                                                                                                                                                                                                                  GIPGVGPFGGPQPGVPL-GYPIKAPKLPG----GYGLPYTTGKLPYGYGPGGV----AGA
                      vgv-pgygypgypgypgygyapgygyapgygyapgygyapgygyapgygyapgygyapgygy-apgy
-GVFYPGAGLGALGGPG-PG-GKPLKPVPG-GLAGAGLGAG
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        GVPG-AIPG-GVPG--
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elastin; repeat sequence; suture; thread; pin; gel; silk;
E.coli; EC3.
                                                                         "polymer repeat block sequence"
                                                               Location/Qualifiers
                                                                                                                      94US-00212237
                                                                                                          95WO-US002772
                                                                       1. .76
/note= '
                          Polymer SELP7
                                                                                                            10-MAR-1995;
                                                                                       WO9524478-A1
                                                                                                 14-SEP-1995
                                                      Synthetic.
                                     Fibroin;
                                           polymer;
                                                                      Peptide
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The sequences represented by AAR80251-R80257 are polymers constructed of repeating blocks of fibroin-like (see repeating blocks of fibroin-like (see aAR80250) units. This sequence contains 13 repeats of a block consisting canded and the sequence contains and a block consisting contains of a block consisting and a sequence sencoding these polymers were inserted into plasmids which were sequences encoding these polymers were inserted into plasmids which were used to transform E.coli strain EC3. The polymers could then be isolated to polymers are used to form a device (such as a suture, pin, thread, gel or polymers are used to form a device (such as a suture, pin, thread, gel or confine the two repetative units, and by altering the lengths of the blocks of of the two repetative units, and by altering the lengths of the blocks of cach of them. The tensile properties of the polymer can altered moderatly. By reducing the number of repeating units of this sequence, or by increasing the number of units of the polymers signed (see AAR8025) and the fastest resorption rate. The SELP4 (see AAR8025) and SELP5 (see had the fastest resorption rate. The SELP4 (see AAR8025) and selP5 (see three polymers showed intermediate resorption. No data was given for certain the conternance.
Protein polymer comprising alternating blocks of fibroin and elastin
units - used to form a device e.g. a suture to keep separated viable
                                                                                                                                 Example 1; Page 27-30; 46pp; English.
                                                                                 tissue together.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SELP6
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Sequence 988 AA;

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441
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                                                                                                                                                                                                                                                                                                          286 KAAKYGAAAGLVPG+----GPGFGPGVVGVPGAGVPGVGVPGAGIP--VVPGAGIPGAAV 338
                                                                                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                                                                                                                                                                                                                          467
                                                                                                                                                                                                                                                               KAAAKEGAGAAGVLEGVG--GAGVE--GVEG-ALEGIG----GIAGVGTEAAAAAAAAA 285
                                                                                                                                                                                                                                                                                     351
                                                                                                                                                                                                                                                                                                                                 411
                                                                                                                                                  130 AGAGSGAGAGSGAGAGSGAGAGSVÞGVGVPGVGVPGVGVÞGVGVÞGVGVÞGVGV-ÞGVGVPGVGV 188
                                                                                                                                                                                                                                 105
                                                                                                ---IPGVGPFGGPQPGVPL 178
                                                                                                                                                                                                                                                                                                                       GYPIKAPKLPG----GYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAA
                                                                                                                                                                                                                                                                             PGVVSPBAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGV----AGV
                                                                                                                                                                                                                                                                                                                                                                   PSVG----GVPGVG----GVPGVGISPEAQAAAAAKAAKYGVGTPAAAAKA----AAK
                                                                                    49 LGAGLGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ-
                                                                                                                              -------PGAGVKPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGV
                                                                                                                                                                                             Gaps
                    Mismatches 187; Indels 130;
Length 988;
                                           2 GVPG-AIPG-GVPG----GVFYPGAGLGALGGGALGPG-
 33.2%; Score 890; DB 2; 42.4%; Pred. No. 1.8e-45;
                         34;
                                                                                                                                                                              KPKAPGVGGAFAG-----
                          258; Conservative
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         395
                                                                                                                                                                                                                                                                                                                                                                                                                              468
                                                                                                                                                                                                                                                                                                                                                                                                                                                    442
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                                                                                                                                       106
                            Matches
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PROT-) PROTEIN POLYMER TECHNOLOGIES INC

11-MAR-1994;

WPI; 1995-328270/42.

Cappello J;

234

285

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286 KAAKYGAAAGLVPG-----GPGFGPGVVGVPGAGVPGVGVPGAGIP---VVPGAGIPGAAV 338
                                                                                                                                                                                                                                                       PGVVSPEAAAKAAAKAGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGV----AGV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVGVPGVGGAGAGSGAGAGSGAGAGSGA----GAGSGAGAGSGAGAGSVPGVPGVPGVGV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSVG----GVPGVG----GVPGVGISPEAQAAAAKAAKYGVGTPAAAAKA-----AAK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGTGPGGGGVAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 GAGAGSVPGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGA-PGVGG-PGVG 579
                                                                                                                                 GYPIKAPKLPG----GYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVGPQAAAAAA
                                                                                                                                                                235 KAAAKFGAGAAGVLPGVG--GAGVP--GVPG-ALPGIG----GIAGVGTPAAAAAAAAAA
                                                                                       ----PGVGGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSVPGVGV---PGVGVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein polymer comprising alternating blocks of fibroin and elastin
units - used to form a device e.g. a suture to keep separated viable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .64
/note= "polymer repeat block sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 25-27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR80252 standard; peptide; 832 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00212237.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                            150 KPKAPGVGGAFAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 AKSAAKVAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 AGAGSGAGA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymer; E.coli, EC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-328270/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue together.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymer SELP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                      179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        412
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition (C1) comprising: (a) a protein polymer of at least 15kDa which comprises alternating blocks of at least 2 units each of a sequence of 3.30 amino acids which promotes protein crystallisation, and an amino acid sequence which is an elastin-like element, a collagen-like element or a keratin-like element, and (b) a biologically active substance. The composition acquires a non-liquid form under physiological conditions. Also described: (1) delivering a biologically active substance to a localized site in vivo, comprising a diministering C1, where the biologically active substance is delivered from the non-liquid to the localized site; and (2) altering the physical from the non-liquid to the localized site; and (2) altering the physical composition is used for the compression administering a C1.

The composition is used for the controlled release of biologically active compounds in vivo. It can also be used to alter the physical dimensions of a body tissue. The present sequence represents a protein polymer block amino acid sequence from the present invention
                                                                                                                                                                                                                                                                                                   Protein crystallisation; elastin; collagen; keratin; controlled release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising a repetitive polymer containing alternating blocks of sequences that promote protein crystallization and sequences that are elastin, collagen or keratin-like elements, useful for in vivo drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 LGAGLGAFPAVTFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GKPLKPVPGGLAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Mismatches 187; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 988;
                                                                                                                                                                                                                                                         Protein polymer SELP7 polymer block amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.2%; Score 890; DB 5; 42.4%; Pred. No. 1.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 22; 32pp; English.
                                                                                                                     ABP53474 standard; protein; 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00806029
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                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stedronsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEDRONSKY E R.
       AGAGSGAGA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-681318/73.
                                                                                                                                                                                                                                                                                                                             physical dimension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAPP/) CAPPELLO J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  US2002045567-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 988 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1997;
                                                                                                                                                                                                               20-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cappello J,
                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                    ABP53474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
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Matches
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the sequences teptescented by Annovesi-roves, are polygicis consistuated of repeating blocks of fibroin-like (see AAR80249) and elastin-like (see AAR80250) units. This sequence contains 13 repeats of a block consisting of 8 elastin-like repeats followed by 4 fibroin-like repeats. The DNA consisting sequences encoding these polymers were inserted into plasmids which were used to transform E.coli strain EG3. The polymers could then be isolated from the fermented strains by standard centrifugation techniques. The polymers are used to form a device (such as a suture, pin, thread, gel or film) to keep separated viable tissue together. By varying the the ratio of the two repetative units, and by altering the lengths of the blocks of cach of them, the tensile properties of the polymer can altered moderatly. By reducing the number of repeating units of this sequence, or by increasing the number of units of the polymers afaster by increasing the number of the search like repeat, a faster of rate of resorption can be achieved. Of the polymers SELPO (see AAR80251) and the fastest resorption rate. The SELP4 (see AAR80255) and SELP5 (see AAR80255) polymers showed intermediate resorption. No data was given for three forms.) sequences represented by AAR80251-R80257 are polymers constructed of (see AAR80257 three J SELP6

Sequence 832 AA;

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41;
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                                                                                                              FPAVIFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ----PGAGV 110
                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                                                                                                                                                 GVPGV-GVPGVPGVPGVGGAGAGAGAGAGAGAGA---SGAGAGSVPG-VGVPGVPGVF 335
                                                                                                                                                                                                                                                                                           PG-GVAGAAGKAGYPTGTGVGPQAAAAAAKAAAKFGAGAAGV-LPGVG--GAGVPGVPG 261
                                                       55
                                                                                    64
                                                                                                                                                                                                                                                                                                            AIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGPGFG--PGVVGVPGAGVPGVG
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                                                                                  GVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGGAGGAGSGAG-----AGSGAGAGSGAGAGS
                                                                                                                                           --GVFYPGAGLGALGGGGALGPGGKPLKPVPGGLAGAGLGAGLGA
                                                                                                                                                                          KPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGVKPKAPGVGGAFAG-----
                                                                                                                                                                                                                                    ---IPGVG--PFGGPQPGVP-LGYPIKAPKLPGGYGLPYTTGKLPYGYG-
                                                                                                                                                                                                                                                                -----GNGV
                             Gaps
32.5%; Score 872; DB 2; Length 832;
46.5%; Pred. No. 1.8e-44;
ive 30; Mismatches 161; Indels 106;
                                                                                                                                                                                                                                                                SGAGAGSGAGAGSVPĠVĠVPGVĠVPGVĠVPGVĠVP-----ĠVĠVP
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                Best Local Similarity 46.5
Matches 258; Conservative
                                                           GVPG-AIPG-GVPG--
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The present invention describes a composition (CI) comprising: (a) a protein polymer of at least 15kDa which comprises alternating blocks of at least 2 units each of a sequence of 3-30 amino acids which promotes or protein crystallisation, and an amino acid sequence which is an elasting like element, a collagen-like element or a keratin-like element, and (b) like element, a collagen-like element or a keratin-like element; and (b) composition acquires a non-liquid composition acquires a non-liquid composition acquires a non-liquid composition acquires a non-liquid composition acquires a non-liquid composition acquires a non-liquid composition acquires a non-liquid composition and administering a composition is used for the localized site in vivo, comprising all composition is used for the controlled release of biologically active compounds in vivo. It can also be used to alter the physical dimensions compounds in vivo. It can also be used to alter the physical dimensions of a manner of a present sequence represents a protein polymer block are not alter the physical dimensions of a proper present a sequence represents a protein polymer block are presented and account of the present and account of the present a protein polymer block are not account of the present a protein polymer block are not account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account of the present and account 
                                                                                           Protein crystallisation; elastin; collagen; keratin; controlled release;
physical dimension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        blocks of sequences that promote protein crystallization and sequences that are elastin, collagen or keratin-like elements, useful for in vivo drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         composition comprising a repetitive polymer containing alternating
                                               Protein polymer SELP8 polymer block amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Page 22; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             97US-00806029
                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-00806029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ER;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cappello J, Stedronsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPPELLO J.
STEDRONSKY E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-681318/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 832 AA;
                                                                                                                                                                                                                                                                            US2002045567-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-1997;
20-NOV-2002
                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAPP/)
(STED/)
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205 PG-GVAGAAGKAGYPTGTGVGPQAAAAAAAAAKFGAGAAGV-LPGVG--GAGVPGVPG 261 162 64 56 FPAVTFPGALVPGGVADAAAYKAAKAGAGLG--GVPGVGGLGVSAGAVVPQ---PGAGV 111 KPGKVPGVGLPGV-YPGGVLPGARFPGVGVLPGVPT-GAGVKPKAPGVGGAFAG-----125 GAĠSVÞĠVĠVPĠVGVÞĠVGVPĠVGVPĠVĠV-ÞĠVGVPĠVĠV----ÞĠVĠĠĀĠĀĠĀGAGĀG 10 GVPGVGVPGVGVPGVGVPGVGVPGVGGAGAGAGAGAGGAGG-----AGSGAGAGAGAGAGAGAG ASAB------GAGA --IPGVG--PFGGPQPGVP-LGYPIKAPKLPGGYGLPYTTGKLPYGYG-GVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGLGA Indels 106; 32.5%; Score 872; DB 5; Length 832; 46.5%; Pred. No. 1.8e-44; rive 30; Mismatches 161; Indels 1 SGAGAGSGAGAGSVPGVGVPGVGVPGVGVPGVGVP-----GVGVP-2 GVPG-AIPG-GVPG--Conservative Query Match Best Local Similarity Matches 258; Conserv 180 224 163 206 g g

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ABP53473 standard; protein; 832

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